

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 7940X
- (i) APPLICANT: Artavanis-Tsakonas, S. et al.
- (ii) TITLE OF INVENTION: Therapeutic And Diagnostic Methods  
And Compositions Based On Notch Proteins And  
Nucleic Acids
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- B
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/083,590  
(B) FILING DATE: 25-JUN-1993  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Misrock, S. Leslie  
(B) REGISTRATION NUMBER: 18,872  
(C) REFERENCE/DOCKET NUMBER: 7326-015
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 212 790-9090  
(B) TELEFAX: 212 8698864/9741  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2892 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 142..2640

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA 60

CACACACAC CACAGCCCGT GGATTATTAC ACTAAAAGCG AACTCAATC CAAAAAATCA 120

GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA 171

Met His Trp Ile Lys Cys Leu Leu Thr Ala																
1 5 10																
TTC	ATT	TGC	TTC	ACA	GTC	ATC	GTG	CAG	GTT	CAC	AGT	TCC	GGC	AGC	TTT	219
Phe	Ile	Cys	Phe	Thr	Val	Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	
				15					20					25		
GAG	TTG	CGC	CTG	AAG	TAC	TTC	AGC	AAC	GAT	CAC	GGG	CGG	GAC	AAC	GAG	267
Glu	Leu	Arg	Leu	Lys	Tyr	Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	
			30					35					40			
GGT	CGC	TGC	TGC	AGC	GGG	GAG	TCG	GAC	GGA	GCG	ACG	GGC	AAG	TGC	CTG	315
Gly	Arg	Cys	Cys	Ser	Gly	Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	
		45					50					55				
GGC	AGC	TGC	AAG	ACG	CGG	TTT	CGC	GTC	TGC	CTA	AAG	CAC	TAC	CAG	GCC	363
Gly	Ser	Cys	Lys	Thr	Arg	Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	
	60					65					70					
ACC	ATC	GAC	ACC	ACC	TCC	CAG	TGC	ACC	TAC	GGG	GAC	GTG	ATC	ACG	CCC	411
Thr	Ile	Asp	Thr	Thr	Ser	Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	
	75				80					85					90	
ATT	CTC	GGC	GAG	AAC	TCG	GTC	AAT	CTG	ACC	GAC	GCC	CAG	CGC	TTC	CAG	459
Ile	Leu	Gly	Glu	Asn	Ser	Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	
				95					100					105		
AAC	AAG	GGC	TTC	ACG	AAT	CCC	ATC	CAG	TTC	CCC	TTC	TCG	TTC	TCA	TGG	507
Asn	Lys	Gly	Phe	Thr	Asn	Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	
			110					115					120			
CCG	GGT	ACC	TTC	TCG	CTG	ATC	GTC	GAG	GCC	TGG	CAT	GAT	ACG	AAC	AAT	555
Pro	Gly	Thr	Phe	Ser	Leu	Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	
		125					130					135				
AGC	GGC	AAT	GCG	CGA	ACC	AAC	AAG	CTC	CTC	ATC	CAG	CGA	CTC	TTG	GTG	603
Ser	Gly	Asn	Ala	Arg	Thr	Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	
	140					145					150					
CAG	CAG	GTA	CTG	GAG	GTG	TCC	TCC	GAA	TGG	AAG	ACG	AAC	AAG	TCG	GAA	651
Gln	Gln	Val	Leu	Glu	Val	Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	
	155				160					165					170	
TCG	CAG	TAC	ACG	TCG	CTG	GAG	TAC	GAT	TTC	CGT	GTC	ACC	TGC	GAT	CTC	699
Ser	Gln	Tyr	Thr	Ser	Leu	Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	
				175					180					185		
AAC	TAC	TAC	GGA	TCC	GGC	TGT	GCC	AAG	TTC	TGC	CGG	CCC	CGC	GAC	GAT	747
Asn	Tyr	Tyr	Gly	Ser	Gly	Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	
			190					195					200			
TCA	TTT	GGA	CAC	TCG	ACT	TGC	TCG	GAG	ACG	GGC	GAA	ATT	ATC	TGT	TTG	795
Ser	Phe	Gly	His	Ser	Thr	Cys	Ser	Glu	Thr	Gly	Glu	Ile	Ile	Cys	Leu	
		205					210					215				
ACC	GGA	TGG	CAG	GGC	GAT	TAC	TGT	CAC	ATA	CCC	AAA	TGC	GCC	AAA	GGC	843
Thr	Gly	Trp	Gln	Gly	Asp	Tyr	Cys	His	Ile	Pro	Lys	Cys	Ala	Lys	Gly	
	220					225					230					
TGT	GAA	CAT	GGA	CAT	TGC	GAC	AAA	CCC	AAT	CAA	TGC	GTT	TGC	CAA	CTG	891
Cys	Glu	His	Gly	His	Cys	Asp	Lys	Pro	Asn	Gln	Cys	Val	Cys	Gln	Leu	
	235				240					245					250	
GGC	TGG	AAG	GGA	GCC	TTG	TGC	AAC	GAG	TGC	GTT	CTG	GAA	CCG	AAC	TGC	939
Gly	Trp	Lys	Gly	Ala	Leu	Cys	Asn	Glu	Cys	Val	Leu	Glu	Pro	Asn	Cys	
				255					260					265		

ATC	CAT	GGC	ACC	TGC	AAC	AAA	CCC	TGG	ACT	TGC	ATC	TGC	AAC	GAG	GGT	987
Ile	His	Gly	Thr	Cys	Asn	Lys	Pro	Trp	Thr	Cys	Ile	Cys	Asn	Glu	Gly	
		270						275					280			
TGG	GGA	GGC	TTG	TAC	TGC	AAC	CAG	GAT	CTG	AAC	TAC	TGC	ACC	AAC	CAC	1035
Trp	Gly	Gly	Leu	Tyr	Cys	Asn	Gln	Asp	Leu	Asn	Tyr	Cys	Thr	Asn	His	
		285					290					295				
AGA	CCC	TGC	AAG	AAT	GGC	GGA	ACC	TGC	TTC	AAC	ACC	GGC	GAG	GGA	TTG	1083
Arg	Pro	Cys	Lys	Asn	Gly	Gly	Thr	Cys	Phe	Asn	Thr	Gly	Glu	Gly	Leu	
	300					305					310					
TAC	ACA	TGC	AAA	TGC	GCT	CCA	GGA	TAC	AGT	GGT	GAT	GAT	TGC	GAA	AAT	1131
Tyr	Thr	Cys	Lys	Cys	Ala	Pro	Gly	Tyr	Ser	Gly	Asp	Asp	Cys	Glu	Asn	
	315				320					325					330	
GAG	ATC	TAC	TCC	TGC	GAT	GCC	GAT	GTC	AAT	CCC	TGC	CAG	AAT	GGT	GGT	1179
Glu	Ile	Tyr	Ser	Cys	Asp	Ala	Asp	Val	Asn	Pro	Cys	Gln	Asn	Gly	Gly	
				335					340					345		
ACC	TGC	ATC	GAT	GAG	CCG	CAC	ACA	AAA	ACC	GGC	TAC	AAG	TGT	CAT	TGC	1227
Thr	Cys	Ile	Asp	Glu	Pro	His	Thr	Lys	Thr	Gly	Tyr	Lys	Cys	His	Cys	
			350					355					360			
GCC	AAC	GGC	TGG	AGC	GGA	AAG	ATG	TGC	GAG	GAG	AAA	GTG	CTC	ACG	TGT	1275
Ala	Asn	Gly	Trp	Ser	Gly	Lys	Met	Cys	Glu	Glu	Lys	Val	Leu	Thr	Cys	
		365					370					375				
TCG	GAC	AAA	CCC	TGT	CAT	CAG	GGA	ATC	TGC	CGC	AAC	GTT	CGT	CCT	GGC	1323
Ser	Asp	Lys	Pro	Cys	His	Gln	Gly	Ile	Cys	Arg	Asn	Val	Arg	Pro	Gly	
	380					385					390					
TTG	GGA	AGC	AAG	GGT	CAG	GGC	TAC	CAG	TGC	GAA	TGT	CCC	ATT	GGC	TAC	1371
Leu	Gly	Ser	Lys	Gly	Gln	Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Ile	Gly	Tyr	
	395				400					405				410		
AGC	GGA	CCC	AAC	TGC	GAT	CTC	CAG	CTG	GAC	AAC	TGC	AGT	CCG	AAT	CCA	1419
Ser	Gly	Pro	Asn	Cys	Asp	Leu	Gln	Leu	Asp	Asn	Cys	Ser	Pro	Asn	Pro	
				415					420					425		
TGC	ATA	AAC	GGT	GGA	AGC	TGT	CAG	CCG	AGC	GGA	AAG	TGT	ATT	TGC	CCA	1467
Cys	Ile	Asn	Gly	Gly	Ser	Cys	Gln	Pro	Ser	Gly	Lys	Cys	Ile	Cys	Pro	
			430					435					440			
GCG	GGA	TTT	TCG	GGA	ACG	AGA	TGC	GAG	ACC	AAC	ATT	GAC	GAT	TGT	CTT	1515
Ala	Gly	Phe	Ser	Gly	Thr	Arg	Cys	Glu	Thr	Asn	Ile	Asp	Asp	Cys	Leu	
		445					450					455				
GGC	CAC	CAG	TGC	GAG	AAC	GGA	GGC	ACC	TGC	ATA	GAT	ATG	GTC	AAC	CAA	1563
Gly	His	Gln	Cys	Glu	Asn	Gly	Gly	Thr	Cys	Ile	Asp	Met	Val	Asn	Gln	
	460					465					470					
TAT	CGC	TGC	CAA	TGC	GTT	CCC	GGT	TTC	CAT	GGC	ACC	CAC	TGT	AGT	AGC	1611
Tyr	Arg	Cys	Gln	Cys	Val	Pro	Gly	Phe	His	Gly	Thr	His	Cys	Ser	Ser	
	475				480					485					490	
AAA	GTT	GAC	TTG	TGC	CTC	ATC	AGA	CCG	TGT	GCC	AAT	GGA	GGA	ACC	TGC	1659
Lys	Val	Asp	Leu	Cys	Leu	Ile	Arg	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	
				495					500					505		
TTG	AAT	CTC	AAC	AAC	GAT	TAC	CAG	TGC	ACC	TGT	CGT	GCG	GGA	TTT	ACT	1707
Leu	Asn	Leu	Asn	Asn	Asp	Tyr	Gln	Cys	Thr	Cys	Arg	Ala	Gly	Phe	Thr	
			510					515					520			
GGC	AAG	GAT	TGC	TCT	GTG	GAC	ATC	GAT	GAG	TGC	AGC	AGT	GGA	CCC	TGT	1755
Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
		525					530					535				

B

CAT His 540	AAC Asn	GGC Gly	GGC Gly	ACT Thr	TGC Cys	ATG Met 545	AAC Asn	CGC Arg	GTC Val	AAT Asn 550	TCG Ser	TTC Phe	GAA Glu	TGC Cys	GTG Val	1803
TGT Cys 555	GCC Ala	AAT Asn	GGT Gly	TTC Phe	AGG Arg 560	GGC Gly	AAG Lys	CAG Gln	TGC Cys	GAT Asp 565	GAG Glu	GAG Glu	TCC Ser	TAC Tyr	GAT Asp 570	1851
TCG Ser	GTG Val	ACC Thr	TTC Phe	GAT Asp 575	GCC Ala	CAC His	CAA Gln	TAT Tyr	GGA Gly 580	GCG Ala	ACC Thr	ACA Thr	CAA Gln	GCG Ala	AGA Arg 585	1899
GCC Ala	GAT Asp	GGT Gly	TTG Leu 590	ACC Thr	AAT Asn	GCC Ala	CAG Gln	GTA Val 595	GTC Val	CTA Leu	ATT Ile	GCT Ala	GTT Val	TTC Phe	TCC Ser	1947
GTT Val	GCG Ala	ATG Met 605	CCT Pro	TTG Leu	GTG Val	GCG Ala	GTT Val 610	ATT Ile	GCG Ala	GCG Ala	TGC Cys	GTG Val	GTC Val	TTC Phe	TGC Cys	1995
ATG Met 620	AAG Lys	CGC Arg	AAG Lys	CGT Arg	AAG Lys	CGT Arg 625	GCT Ala	CAG Gln	GAA Glu	AAG Lys	GAC Asp 630	GAC Asp	GCG Ala	GAG Glu	GCC Ala	2043
AGG Arg 635	AAG Lys	CAG Gln	AAC Asn	GAA Glu	CAG Gln 640	AAT Asn	GCG Ala	GTG Val	GCC Ala	ACA Thr 645	ATG Met	CAT His	CAC His	AAT Asn	GGC Gly 650	2091
AGT Ser	GGG Gly	GTG Val	GGT Gly	GTA Val 655	GCT Ala	TTG Leu	GCT Ala	TCA Ser	GCC Ala 660	TCT Ser	CTG Leu	GGC Gly	GGC Gly	AAA Lys	ACT Thr 665	2139
GGC Gly	AGC Ser	AAC Asn	AGC Ser 670	GGT Gly	CTC Leu	ACC Thr	TTC Phe	GAT Asp 675	GGC Gly	GGC Gly	AAC Asn	CCG Pro	AAT Asn	ATC Ile	ATC Ile	2187
AAA Lys	AAC Asn	ACC Thr 685	TGG Trp	GAC Asp	AAG Lys	TCG Ser	GTC Val 690	AAC Asn	AAC Asn	ATT Ile	TGT Cys	GCC Ala 695	TCA Ser	GCA Ala	GCA Ala	2235
GCA Ala 700	GCG Ala	GCG Ala	GCG Ala	GCA Ala	GCA Ala	GCG Ala 705	GCG Ala	GCG Ala	GAC Asp	GAG Glu	TGT Cys 710	CTC Leu	ATG Met	TAC Tyr	GGC Gly	2283
GGA Gly 715	TAT Tyr	GTG Val	GCC Ala	TCG Ser 720	GTG Val	GCG Ala	GAT Asp	AAC Asn	AAC Asn	AAT Asn 725	GCC Ala	AAC Asn	TCA Ser	GAC Asp	TTT Phe 730	2331
TGT Cys	GTG Val	GCT Ala	CCG Pro	CTA Leu 735	CAA Gln	AGA Arg	GCC Ala	AAG Lys	TCG Ser 740	CAA Gln	AAG Lys	CAA Gln	CTC Leu	AAC Asn	ACC Thr 745	2379
GAT Asp	CCC Pro	ACG Thr	CTC Leu 750	ATG Met	CAC His	CGC Arg	GGT Gly	TCG Ser 755	CCG Pro	GCA Ala	GGC Gly	AGC Ser	TCA Ser	GCC Ala	AAG Lys	2427
GGA Gly	GCG Ala	TCT Ser 765	GGC Gly	GGA Gly	GGA Gly	CCG Pro	GGA Gly 770	GCG Ala	GCG Ala	GAG Glu	GGC Gly	AAG Lys	AGG Arg	ATC Ile	TCT Ser	2475
GTT Val	TTA Leu 780	GGC Gly	GAG Glu	GGT Gly	TCC Ser	TAC Tyr 785	TGT Cys	AGC Ser	CAG Gln	CGT Arg	TGG Trp 790	CCC Pro	TCG Ser	TTG Leu	GCG Ala	2523
GCG Ala 795	GCG Ala	GGA Gly	GTG Val	GCC Ala	GGA Gly	GCC Ala	TGT Cys 800	TCA Ser	TCC Ser	CAG Gln 805	CTA Leu	ATG Met	GCT Ala	GCA Ala	GCT Ala 810	2571

TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val	
815 820 825	
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670
Val Cys Gly Thr Pro His Met	
830	
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTTG ATTGAAGCAG TTTAGTCGTC	2790
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

B

Met	His	Trp	Ile	Lys	Cys	Leu	Leu	Thr	Ala	Phe	Ile	Cys	Phe	Thr	Val
1				5					10					15	
Ile	Val	Gln	Val	His	Ser	Ser	Gly	Ser	Phe	Glu	Leu	Arg	Leu	Lys	Tyr
			20					25					30		
Phe	Ser	Asn	Asp	His	Gly	Arg	Asp	Asn	Glu	Gly	Arg	Cys	Cys	Ser	Gly
		35					40					45			
Glu	Ser	Asp	Gly	Ala	Thr	Gly	Lys	Cys	Leu	Gly	Ser	Cys	Lys	Thr	Arg
	50					55					60				
Phe	Arg	Val	Cys	Leu	Lys	His	Tyr	Gln	Ala	Thr	Ile	Asp	Thr	Thr	Ser
65					70				75						80
Gln	Cys	Thr	Tyr	Gly	Asp	Val	Ile	Thr	Pro	Ile	Leu	Gly	Glu	Asn	Ser
				85					90					95	
Val	Asn	Leu	Thr	Asp	Ala	Gln	Arg	Phe	Gln	Asn	Lys	Gly	Phe	Thr	Asn
			100					105					110		
Pro	Ile	Gln	Phe	Pro	Phe	Ser	Phe	Ser	Trp	Pro	Gly	Thr	Phe	Ser	Leu
		115					120					125			
Ile	Val	Glu	Ala	Trp	His	Asp	Thr	Asn	Asn	Ser	Gly	Asn	Ala	Arg	Thr
	130					135					140				
Asn	Lys	Leu	Leu	Ile	Gln	Arg	Leu	Leu	Val	Gln	Gln	Val	Leu	Glu	Val
145					150					155					160
Ser	Ser	Glu	Trp	Lys	Thr	Asn	Lys	Ser	Glu	Ser	Gln	Tyr	Thr	Ser	Leu
				165					170					175	
Glu	Tyr	Asp	Phe	Arg	Val	Thr	Cys	Asp	Leu	Asn	Tyr	Tyr	Gly	Ser	Gly
		180						185					190		
Cys	Ala	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Ser	Phe	Gly	His	Ser	Thr
		195					200					205			

Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp  
 210 215 220  
 Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys  
 225 230 235 240  
 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu  
 245 250 255  
 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn  
 260 265 270  
 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys  
 275 280 285  
 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly  
 290 295 300  
 Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu Tyr Thr Cys Lys Cys Ala  
 305 310 315 320  
 Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn Glu Ile Tyr Ser Cys Asp  
 325 330 335  
 Ala Asp Val Asn Pro Cys Gln Asn Gly Gly Thr Cys Ile Asp Glu Pro  
 340 345 350  
 His Thr Lys Thr Gly Tyr Lys Cys His Cys Ala Asn Gly Trp Ser Gly  
 355 360 365  
 Lys Met Cys Glu Glu Lys Val Leu Thr Cys Ser Asp Lys Pro Cys His  
 370 375 380  
 Gln Gly Ile Cys Arg Asn Val Arg Pro Gly Leu Gly Ser Lys Gly Gln  
 385 390 395 400  
 Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr Ser Gly Pro Asn Cys Asp  
 405 410 415  
 Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro Cys Ile Asn Gly Gly Ser  
 420 425 430  
 Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro Ala Gly Phe Ser Gly Thr  
 435 440 445  
 Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly His Gln Cys Glu Asn  
 450 455 460  
 Gly Gly Thr Cys Ile Asp Met Val Asn Gln Tyr Arg Cys Gln Cys Val  
 465 470 475 480  
 Pro Gly Phe His Gly Thr His Cys Ser Ser Lys Val Asp Leu Cys Leu  
 485 490 495  
 Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys Leu Asn Leu Asn Asn Asp  
 500 505 510  
 Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr Gly Lys Asp Cys Ser Val  
 515 520 525  
 Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys His Asn Gly Gly Thr Cys  
 530 535 540  
 Met Asn Arg Val Asn Ser Phe Glu Cys Val Cys Ala Asn Gly Phe Arg  
 545 550 555 560  
 Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp Ser Val Thr Phe Asp Ala

B

99

565 570 575

His Gln Tyr Gly Ala Thr Thr Gln Ala Arg Ala Asp Gly Leu Thr Asn  
580 585 590

Ala Gln Val Val Leu Ile Ala Val Phe Ser Val Ala Met Pro Leu Val  
595 600 605

Ala Val Ile Ala Ala Cys Val Val Phe Cys Met Lys Arg Lys Arg Lys  
610 615 620

Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala Arg Lys Gln Asn Glu Gln  
625 630 635 640

Asn Ala Val Ala Thr Met His His Asn Gly Ser Gly Val Gly Val Ala  
645 650 655

Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr Gly Ser Asn Ser Gly Leu  
660 665 670

Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile Lys Asn Thr Trp Asp Lys  
675 680 685

Ser Val Asn Asn Ile Cys Ala Ser Ala Ala Ala Ala Ala Ala Ala  
690 695 700

Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly Gly Tyr Val Ala Ser Val  
705 710 715 720

Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe Cys Val Ala Pro Leu Gln  
725 730 735

Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr Asp Pro Thr Leu Met His  
740 745 750

Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys Gly Ala Ser Gly Gly Gly  
755 760 765

Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser Val Leu Gly Glu Gly Ser  
770 775 780

Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala Ala Ala Gly Val Ala Gly  
785 790 795 800

Ala Cys Ser Ser Gln Leu Met Ala Ala Ala Ser Ala Ala Gly Ser Gly  
805 810 815

Ala Gly Thr Ala Gln Gln Gln Arg Ser Val Val Cys Gly Thr Pro His  
820 825 830

Met

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 442..1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCCTT TTCTGTCAAC GCTAAAGATC	60
TACAAAACAT CAGCGCCTAT CAAGTGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
CCAAATCTG CATACTGGG CTAATTAAGG CTGCCCAGCG AATTACATT TGTGTGGTGC	360
CAATCCAGAG TGAATCCGAA ACAAATCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA	471
Met Phe Arg Lys His Phe Arg Arg Lys Pro	
1 5 10	
GCT ACG TCG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG	519
Ala Thr Ser Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu	
15 20 25	
GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG	567
Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg	
30 35 40	
GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA	615
Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser	
45 50 55	
TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC	663
Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Val	
60 65 70	
CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711
His Lys Ile Ser Ala Ala Gly Asn Phe Glu Leu Glu Ile Leu Glu Ile	
75 80 85 90	
TCA AAT ACC AAC AGC CAT CTA CTC AAC GGC TAT TGC TGC GGC ATG CCA	759
Ser Asn Thr Asn Ser His Leu Leu Asn Gly Tyr Cys Cys Gly Met Pro	
95 100 105	
GCG GAA CTT AGG GCC ACC AAG ACG ATA GGC TGC TCG CCA TGC ACG ACG	807
Ala Glu Leu Arg Ala Thr Lys Thr Ile Gly Cys Ser Pro Cys Thr Thr	
110 115 120	
GCA TTC CGG CTG TGC CTG AAG GAG TAC CAG ACC ACG GAG CAG GGT GCC	855
Ala Phe Arg Leu Cys Leu Lys Glu Tyr Gln Thr Thr Glu Gln Gly Ala	
125 130 135	
AGC ATA TCC ACG GGC TGT TCG TTT GGC AAC GCC ACC ACC AAG ATA CTG	903
Ser Ile Ser Thr Gly Cys Ser Phe Gly Asn Ala Thr Thr Lys Ile Leu	
140 145 150	
GGT GGC TCC AGC TTT GTG CTC AGC GAT CCG GGT GTG GGA GCC ATT GTG	951
Gly Gly Ser Ser Phe Val Leu Ser Asp Pro Gly Val Gly Ala Ile Val	
155 160 165 170	
CTG CCC TTT ACG TTT CGT TGG ACG AAG TCG TTT ACG CTG ATA CTG CAG	999
Leu Pro Phe Thr Phe Arg Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln	
175 180 185	
GCG TTG GAT ATG TAC AAC ACA TCC TAT CCA GAT GCG GAG AGG TTA ATT	1047



Ala	Leu	Asp	Met	Tyr	Asn	Thr	Ser	Tyr	Pro	Asp	Ala	Glu	Arg	Leu	Ile		
			190					195					200				
GAG	GAA	ACA	TCA	TAC	TCG	GGC	GTG	ATA	CTG	CCG	TCG	CCG	GAG	TGG	AAG	1095	
Glu	Glu	Thr	Ser	Tyr	Ser	Gly	Val	Ile	Leu	Pro	Ser	Pro	Glu	Trp	Lys		
		205				210						215					
ACG	CTG	GAC	CAC	ATC	GGG	CGG	AAC	GCG	CGG	ATC	ACC	TAC	CGT	GTC	CGG	1143	
Thr	Leu	Asp	His	Ile	Gly	Arg	Asn	Ala	Arg	Ile	Thr	Tyr	Arg	Val	Arg		
	220				225						230						
GTG	CAA	TGC	GCC	GTT	ACC	TAC	TAC	AAC	ACG	ACC	TGC	ACG	ACC	TTC	TGC	1191	
Val	Gln	Cys	Ala	Val	Thr	Tyr	Tyr	Asn	Thr	Thr	Cys	Thr	Thr	Phe	Cys		
235					240					245					250		
CGT	CCG	CGG	GAC	GAT	CAG	TTC	GGT	CAC	TAC	GCC	TGC	GGC	TCC	GAG	GGT	1239	
Arg	Pro	Arg	Asp	Asp	Gln	Phe	Gly	His	Tyr	Ala	Cys	Gly	Ser	Glu	Gly		
			255						260					265			
CAG	AAG	CTC	TGC	CTG	AAT	GGC	TGG	CAG	GGC	GTC	AAC	TGC	GAG	GAG	GCC	1287	
Gln	Lys	Leu	Cys	Leu	Asn	Gly	Trp	Gln	Gly	Val	Asn	Cys	Glu	Glu	Ala		
			270					275					280				
ATA	TGC	AAG	GCG	GGC	TGC	GAC	CCC	GTC	CAC	GGC						1320	
Ile	Cys	Lys	Ala	Gly	Cys	Asp	Pro	Val	His	Gly							
		285					290										

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Arg	Lys	His	Phe	Arg	Arg	Lys	Pro	Ala	Thr	Ser	Ser	Ser	Leu		
1				5					10					15			
Glu	Ser	Thr	Ile	Glu	Ser	Ala	Asp	Ser	Leu	Gly	Met	Ser	Lys	Lys	Thr		
			20					25					30				
Ala	Thr	Lys	Arg	Gln	Arg	Pro	Arg	His	Arg	Val	Pro	Lys	Ile	Ala	Thr		
		35				40						45					
Leu	Pro	Ser	Thr	Ile	Arg	Asp	Cys	Arg	Ser	Leu	Lys	Ser	Ala	Cys	Asn		
	50					55					60						
Leu	Ile	Ala	Leu	Ile	Leu	Ile	Leu	Val	His	Lys	Ile	Ser	Ala	Ala			
65				70					75					80			
Gly	Asn	Phe	Glu	Leu	Glu	Ile	Leu	Glu	Ile	Ser	Asn	Thr	Asn	Ser	His		
			85					90					95				
Leu	Leu	Asn	Gly	Tyr	Cys	Cys	Gly	Met	Pro	Ala	Glu	Leu	Arg	Ala	Thr		
		100						105					110				
Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu		
		115					120					125					
Lys	Glu	Tyr	Gln	Thr	Thr	Glu	Gln	Gly	Ala	Ser	Ile	Ser	Thr	Gly	Cys		
	130					135					140						
Ser	Phe	Gly	Asn	Ala	Thr	Thr	Lys	Ile	Leu	Gly	Gly	Ser	Ser	Phe	Val		

145		150		155		160
Leu Ser Asp Pro Gly Val Gly Ala Ile Val Leu Pro Phe Thr Phe Arg	165		170		175	
Trp Thr Lys Ser Phe Thr Leu Ile Leu Gln Ala Leu Asp Met Tyr Asn	180		185		190	
Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser	195		200		205	
Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly	210		215		220	
Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr	225		230		235	240
Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln	245		250		255	
Phe Gly His Tyr Ala Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn	260		265		270	
Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys	275		280		285	
Asp Pro Val His Gly	290					

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCTCGGGAA CGGGGGGTAA CACTGAAAGG	60
TCGAGTACCC ATTTCCGTCA TAACGGGTTG GTCGCCCCCT AGGGGTCGGA GTCAGGTGGA	120
CGGGAGGTCG ACAACGCCCG GGGGACGGGT GGTACATGGT GTAAGGTCTT TACCGGACCG	180
GGCAAACGGG TCACACCGAA AGGGGTGAAC GGTAAC TACG GGGTCGTCCT GCCCGTCCAT	240
CGAGTCTGGT AAGAGGGTCG CCTTAAG	267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCTTC CATTATACGT GACTTTTCTG AAAGTGTAGC CACCCTAGTG TCTCTAACTC	60
CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
AACCCGGAAC TGAAGGCTGG CTCTCACCCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
TGTTAGATGT GAATGTCCGT GGCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC	300
GAGGAGGCAG CTCAGATTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
GATGGCCCTG CACCTTGACG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCGCG TGTCCACTCC ATGCTGCAGT	540
GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTGAAAAA TGGGGCCAAC CGAGACATGC	240
AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCCG GGAGGAGCTA TAAGC	295

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180

GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG 240  
CAGAGCTG 248

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNNA GTGCGAGGGA CATTCTGTCG 60  
ACCAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG 120  
GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCGA CAGTCGGTAA 180  
GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTGCGGGCG AGACTCGGGC TCGGGTCAGG 240  
CGGCCTTAAG GACGTCGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GCGCCACCT 300  
CGAGGNCGAA AACAGGGAA ATC 323

B  
(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..3234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 48  
Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn  
1 5 10 15  
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96  
His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp  
20 25 30  
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 144  
Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser  
35 40 45  
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192  
Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp  
50 55 60  
GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240

Gly 65	Phe	Asp	Cys	Gln	Arg 70	Ala	Glu	Gly	Gln	Cys 75	Asn	Pro	Leu	Tyr	Asp 80	
CAG Gln	TAC Tyr	TGC Cys	AAG Lys	GAC Asp 85	CAC His	TTC Phe	AGC Ser	GAC Asp	GGG Gly 90	CAC His	TGC Cys	GAC Asp	CAG Gln	GGC Gly 95	TGC Cys	288
AAC Asn	AGC Ser	GCG Ala	GAG Glu 100	TGC Cys	GAG Glu	TGG Trp	GAC Asp	GGG Gly 105	CTG Leu	GAC Asp	TGT Cys	GCG Ala	GAG Glu 110	CAT His	GTA Val	336
CCC Pro	GAG Glu	AGG Arg 115	CTG Leu	GCG Ala	GCC Ala	GGC Gly	ACG Thr 120	CTG Leu	GTG Val	GTG Val	GTG Val	GTG Val	CTG Leu 125	ATG Met	CCG Pro	384
CCG Pro	GAG Glu 130	CAG Gln	CTG Leu	CGC Arg	AAC Asn 135	AGC Ser 135	TCC Ser	TTC Phe	CAC His	TTC Phe	CTG Leu 140	CGG Arg	GAG Glu	CTC Leu	AGC Ser	432
CGC Arg 145	GTG Val	CTG Leu	CAC His	ACC Thr	AAC Asn 150	GTG Val	GTC Val	TTC Phe	AAG Lys	CGT Arg 155	GAC Asp	GCA Ala	CAC His	GGC Gly	CAG Gln 160	480
CAG Gln	ATG Met	ATC Ile	TTC Phe	CCC Pro 165	TAC Tyr	TAC Tyr	GGC Gly	CGC Arg	GAG Glu 170	GAG Glu	GAG Glu	CTG Leu	CGC Arg	AAG Lys 175	CAC His	528
CCC Pro	ATC Ile	AAG Lys 180	CGT Arg	GCC Ala	GCC Ala	GAG Glu	GGC Gly	TGG Trp 185	GCC Ala	GCA Ala	CCT Pro	GAC Asp	GCC Ala 190	CTG Leu	CTG Leu	576
GGC Gly	CAG Gln 195	GTG Val	AAG Lys	GCC Ala	TCG Ser	CTG Leu	CTC Leu 200	CCT Pro	GGT Gly	GGC Gly	AGC Ser	GAG Glu 205	GGT Gly	GGG Gly	CGG Arg	624
CGG Arg 210	CGG Arg	AGG Arg	GAG Glu	CTG Leu	GAC Asp	CCC Pro 215	ATG Met	GAC Asp	GTC Val	CGC Arg	GGC Gly 220	TCC Ser	ATC Ile	GTC Val	TAC Tyr	672
CTG Leu 225	GAG Glu	ATT Ile	GAC Asp	AAC Asn 230	CGG Arg 230	CAG Gln	TGT Cys	GTG Val	CAG Gln	GCC Ala 235	TCC Ser	TCG Ser	CAG Gln	TGC Cys	TTC Phe 240	720
CAG Gln	AGT Ser	GCC Ala	ACC Thr	GAC Asp 245	GTG Val	GCC Ala	GCA Ala	TTC Phe	CTG Leu 250	GGA Gly	GCG Ala	CTC Leu	GCC Ala	TCG Ser 255	CTG Leu	768
GGC Gly	AGC Ser	CTC Leu	AAC Asn 260	ATC Ile	CCC Pro	TAC Tyr	AAG Lys	ATC Ile 265	GAG Glu	GCC Ala	GTG Val	CAG Gln	AGT Ser 270	GAG Glu	ACC Thr	816
GTG Val	GAG Glu	CCG Pro 275	CCC Pro	CCG Pro	CCG Pro	GCG Ala	CAG Gln 280	CTG Leu	CAC His	TTC Phe	ATG Met	TAC Tyr 285	GTG Val	GCG Ala	GCG Ala	864
GCC Ala 290	GCC Ala	TTT Phe	GTG Val	CTT Leu	CTG Leu	TTC Phe 295	TTC Phe	GTG Val	GGC Gly	TGC Cys	GGG Gly 300	GTG Val	CTG Leu	CTG Leu	TCC Ser	912
CGC Arg 305	AAG Lys	CGC Arg	CGG Arg	CGG Arg	CAG Gln 310	CAT His	GGC Gly	CAG Gln	CTC Leu	TGG Trp 315	TTC Phe	CCT Pro	GAG Glu	GGC Gly 320	TTC Phe 320	960
AAA Lys	GTG Val	TCT Ser	GAG Glu	GCC Ala 325	AGC Ser	AAG Lys	AAG Lys	AAG Lys	CGG Arg 330	CGG Arg	GAG Glu	CCC Pro	CTC Leu	GGC Gly 335	GAG Glu	1008

B

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GAC Asp	TCC Ser	GTG Val	GGC Gly 340	CTC Leu	AAG Lys	CCC Pro	CTG Leu	AAG Lys 345	AAC Asn	GCT Ala	TCA Ser	GAC Asp	GGT Gly 350	GCC Ala	CTC Leu	1056
ATG Met	GAC Asp	GAC Asp 355	AAC Asn	CAG Gln	AAT Asn	GAG Glu	TGG Trp 360	GGG Gly	GAC Asp	GAG Glu	GAC Asp	CTG Leu 365	GAG Glu	ACC Thr	AAG Lys	1104
AAG Lys	TTC Phe 370	CGG Arg	TTC Phe	GAG Glu	GAG Glu	CCC Pro 375	GTG Val	GTT Val	CTG Leu	CCT Pro	GAC Asp 380	CTG Leu	GAC Asp	GAC Asp	CAG Gln	1152
ACA Thr 385	GAC Asp	CAC His	CGG Arg	CAG Gln	TGG Trp 390	ACT Thr	CAG Gln	CAG Gln	CAC His	CTG Leu 395	GAT Asp	GCC Ala	GCT Ala	GAC Asp	CTG Leu 400	1200
CGC Arg	ATG Met	TCT Ser	GCC Ala 405	ATG Met	GCC Ala	CCC Pro	ACA Thr	CCG Pro	CCC Pro 410	CAG Gln	GGT Gly	GAG Glu	GTT Val	GAC Asp 415	GCC Ala	1248
GAC Asp	TGC Cys	ATG Met 420	GAC Asp	GTC Val	AAT Asn	GTC Val	CGC Arg	GGG Gly 425	CCT Pro	GAT Asp	GGC Gly	TTC Phe	ACC Thr 430	CCG Pro	CTC Leu	1296
ATG Met	ATC Ile	GCC Ala 435	TCC Ser	TGC Cys	AGC Ser	GGG Gly	GGC Gly 440	GGC Gly	CTG Leu	GAG Glu	ACG Thr	GGC Gly 445	AAC Asn	AGC Ser	GAG Glu	1344
GAA Glu 450	GAG Glu	GAG Glu	GAC Asp	GCG Ala	CCG Pro	GCC Ala 455	GTC Val	ATC Ile	TCC Ser	GAC Asp	TTC Phe 460	ATC Ile	TAC Tyr	CAG Gln	GGC Gly	1392
GCC Ala 465	AGC Ser	CTG Leu	CAC His	AAC Asn	CAG Gln 470	ACA Thr	GAC Asp	CGC Arg	ACG Thr	GGC Gly 475	GAG Glu	ACC Thr	GCC Ala	TTG Leu	CAC His 480	1440
CTG Leu	GCC Ala	GCC Ala	CGC Arg 485	TAC Tyr	TCA Ser	CGC Arg	TCT Ser	GAT Asp	GCC Ala 490	GCC Ala	AAG Lys	CGC Arg	CTG Leu 495	CTG Leu	GAG Glu	1488
GCC Ala	AGC Ser	GCA Ala 500	GAT Asp	GCC Ala	AAC Asn	ATC Ile	CAG Gln	GAC Asp 505	AAC Asn	ATG Met	GGC Gly	CGC Arg	ACC Thr 510	CCG Pro	CTG Leu	1536
CAT His	GCG Ala	GCT Val 515	GTG Val	TCT Ser	GCC Ala	GAC Asp	GCA Ala 520	CAA Gln	GGT Gly	GTC Val	TTC Phe	CAG Gln 525	ATC Ile	CTG Leu	ATC Ile	1584
CGG Arg 530	AAC Asn	CGA Arg	GCC Ala	ACA Thr	GAC Asp	CTG Leu 535	GAT Asp	GCC Ala	CGC Arg	ATG Met	CAT His 540	GAT Asp	GGC Gly	ACG Thr	ACG Thr	1632
CCA Pro 545	CTG Leu	ATC Ile	CTG Leu	GCT Ala	GCC Ala 550	CGC Arg	CTG Leu	GCC Ala	GTG Val	GAG Glu 555	GGC Gly	ATG Met	CTG Leu	GAG Glu	GAC Asp 560	1680
CTC Leu	ATC Ile	AAC Asn	TCA Ser 565	CAC His	GCC Ala	GAC Asp	GTC Val	AAC Asn	GCC Ala 570	GTA Val	GAT Asp	GAC Asp	CTG Leu	GGC Gly 575	AAG Lys	1728
TCC Ser	GCC Ala	CTG Leu 580	CAC His	TGG Trp	GCC Ala	GCC Ala	GCC Ala	GTG Val 585	AAC Asn	AAT Asn	GTG Val	GAT Asp	GCC Ala 590	GCA Ala	GTT Val	1776
GTG Val	CTC Leu	CTG Leu 595	AAG Lys	AAC Asn	GGG Gly	GCT Ala	AAC Asn 600	AAA Lys	GAT Asp	ATG Met	CAG Gln	AAC Asn 605	AAC Asn	AGG Arg	GAG Glu	1824

GAG Glu 610	ACA Thr	CCC Pro	CTG Leu	TTT Phe	CTG Leu	GCC Ala 615	GCC Ala	CGG Arg	GAG Glu	GGC Gly	AGC Ser 620	TAC Tyr	GAG Glu	ACC Thr	GCC Ala	1872
AAG Lys 625	GTG Val	CTG Leu	CTG Leu	GAC Asp	CAC His 630	TTT Phe	GCC Ala	AAC Asn	CGG Arg	GAC Asp 635	ATC Ile	ACG Thr	GAT Asp	CAT His	ATG Met 640	1920
GAC Asp	CGC Arg	CTG Leu	CCG Pro	CGC Arg 645	GAC Asp	ATC Ile	GCA Ala	CAG Gln	GAG Glu 650	CGC Arg	ATG Met	CAT His	CAC His	GAC Asp 655	ATC Ile	1968
GTG Val	AGG Arg	CTG Leu	CTG Leu 660	GAC Asp	GAG Glu	TAC Tyr	AAC Asn	CTG Leu 665	GTG Val	CGC Arg	AGC Ser	CCG Pro	CAG Gln 670	CTG Leu	CAC His	2016
GGA Gly	GCC Ala	CCG Pro 675	CTG Leu	GGG Gly	GGC Gly	ACG Thr	CCC Pro 680	ACC Thr	CTG Leu	TCG Ser	CCC Pro 685	CCG Pro	CTC Leu	TGC Cys	TCG Ser	2064
CCC Pro 690	AAC Asn	GGC Gly	TAC Tyr	CTG Leu	GGC Gly	AGC Ser 695	CTC Leu	AAG Lys	CCC Pro	GGC Gly	GTG Val 700	CAG Gln	GGC Gly	AAG Lys	AAG Lys	2112
GTC Val 705	CGC Arg	AAG Lys	CCC Pro	AGC Ser	AGC Ser 710	AAA Lys	GGC Gly	CTG Leu	GCC Ala	TGT Cys 715	GGA Gly	AGC Ser	AAG Lys	GAG Glu	GCC Ala 720	2160
AAG Lys	GAC Asp	CTC Leu	AAG Lys	GCA Ala 725	CGG Arg	AGG Arg	AAG Lys	AAG Lys	TCC Ser 730	CAG Gln	GAT Asp	GGC Gly	AAG Lys	GGC Gly 735	TGC Cys	2208
CTG Leu	CTG Leu	GAC Asp 740	AGC Ser	TCC Ser	GGC Gly	ATG Met	CTC Leu	TCG Ser 745	CCC Pro	GTG Val	GAC Asp	TCC Ser	CTG Leu 750	GAG Glu	TCA Ser	2256
CCC Pro	CAT His	GGC Gly 755	TAC Tyr	CTG Leu	TCA Ser	GAC Asp	GTG Val 760	GCC Ala	TCG Ser	CCG Pro	CCA Pro	CTG Leu 765	CTG Leu	CCC Pro	TCC Ser	2304
CCG Pro 770	TTC Phe	CAG Gln	CAG Gln	TCT Ser	CCG Pro	TCC Ser 775	GTG Val	CCC Pro	CTC Leu	AAC Asn	CAC His 780	CTG Leu	CCT Pro	GGG Gly	ATG Met	2352
CCC Pro 785	GAC Asp	ACC Thr	CAC His	CTG Leu	GGC Gly 790	ATC Ile	GGG Gly	CAC His	CTG Leu	AAC Asn 795	GTG Val	GCG Ala	GCC Ala	AAG Lys	CCC Pro 800	2400
GAG Glu	ATG Met	GCG Ala	GCG Ala	CTG Leu 805	GGT Gly	GGG Gly	GGC Gly	GGC Gly	CGG Arg 810	CTG Leu	GCC Ala	TTT Phe	GAG Glu	ACT Thr 815	GGC Gly	2448
CCA Pro	CCT Pro	CGT Arg	CTC Leu 820	TCC Ser	CAC His	CTG Leu	CCT Pro	GTG Val 825	GCC Ala	TCT Ser	GGC Gly	ACC Thr	AGC Ser	ACC Thr	GTC Val	2496
CTG Leu	GGC Gly	TCC Ser 835	AGC Ser	AGC Ser	GGA Gly	GGG Gly	GCC Ala 840	CTG Leu	AAT Asn	TTC Phe	ACT Thr	GTG Val 845	GGC Gly	GGG Gly	TCC Ser	2544
ACC Thr 850	AGT Ser	TTG Leu	AAT Asn	GGT Gly	CAA Gln	TGC Cys 855	GAG Glu	TGG Trp	CTG Leu	TCC Ser	CGG Arg 860	CTG Leu	CAG Gln	AGC Ser	GGC Gly	2592
ATG Met 865	GTG Val	CCG Pro	AAC Asn	CAA Gln	TAC Tyr 870	AAC Asn	CCT Pro	CTG Leu	CGG Arg	GGG Gly 875	AGT Ser	GTG Val	GCA Ala	CCA Pro	GGC Gly 880	2640

CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG	2688
Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro	
885 890 895	
CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC	2736
Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr	
900 905 910	
CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG	2784
Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln	
915 920 925	
ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG	2832
Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu	
930 935 940	
CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA	2880
Gln Pro Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro	
945 950 955 960	
CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG	2928
Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu	
965 970 975	
GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA	2976
Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro	
980 985 990	
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC	3024
Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser	
995 1000 1005	
CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC	3072
Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr	
1010 1015 1020	
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT	3120
Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro	
1025 1030 1035 1040	
GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG	3168
Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met	
1045 1050 1055	
GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC	3216
Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile	
1060 1065 1070	
GAA GCT CCC GAC TCA TGG	3234
Glu Ala Pro Asp Ser Trp	
1075	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys	Gln	Glu	Asp	Ala	Gly	Asn	Lys	Val	Cys	Ser	Leu	Gln	Cys	Asn	Asn
1				5					10					15	

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His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp  
                   20                                  25                                  30  
 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser  
                   35                                  40                                  45  
 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp  
           50                                  55                                  60  
 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp  
   65                                  70                                  75                                  80  
 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys  
                   85                                  90                                  95  
 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val  
                   100                                  105                                  110  
 Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro  
                   115                                  120                                  125  
 Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser  
                   130                                  135                                  140  
 Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln  
   145                                  150                                  155                                  160  
 Gln Met Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His  
                   165                                  170                                  175  
 Pro Ile Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu  
                   180                                  185                                  190  
 Gly Gln Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg  
                   195                                  200                                  205  
 Arg Arg Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr  
                   210                                  215                                  220  
 Leu Glu Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe  
   225                                  230                                  235                                  240  
 Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu  
                   245                                  250                                  255  
 Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr  
                   260                                  265                                  270  
 Val Glu Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala  
                   275                                  280                                  285  
 Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser  
                   290                                  295                                  300  
 Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe  
   305                                  310                                  315                                  320  
 Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu  
                   325                                  330                                  335  
 Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu  
                   340                                  345                                  350  
 Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys  
                   355                                  360                                  365  
 Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln

B

110

370					375					380					
Thr	Asp	His	Arg	Gln	Trp	Thr	Gln	Gln	His	Leu	Asp	Ala	Ala	Asp	Leu
385					390					395					400
Arg	Met	Ser	Ala	Met	Ala	Pro	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala
				405					410					415	
Asp	Cys	Met	Asp	Val	Asn	Val	Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu
			420					425					430		
Met	Ile	Ala	Ser	Cys	Ser	Gly	Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu
		435					440					445			
Glu	Glu	Glu	Asp	Ala	Pro	Ala	Val	Ile	Ser	Asp	Phe	Ile	Tyr	Gln	Gly
	450					455					460				
Ala	Ser	Leu	His	Asn	Gln	Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His
					470					475					480
Leu	Ala	Ala	Arg	Tyr	Ser	Arg	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu
				485					490					495	
Ala	Ser	Ala	Asp	Ala	Asn	Ile	Gln	Asp	Asn	Met	Gly	Arg	Thr	Pro	Leu
			500					505					510		
His	Ala	Ala	Val	Ser	Ala	Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile
		515					520					525			
Arg	Asn	Arg	Ala	Thr	Asp	Leu	Asp	Ala	Arg	Met	His	Asp	Gly	Thr	Thr
	530					535					540				
Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp
	545				550					555					560
Leu	Ile	Asn	Ser	His	Ala	Asp	Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys
				565					570					575	
Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val
			580					585					590		
Val	Leu	Leu	Lys	Asn	Gly	Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Arg	Glu
	595						600					605			
Glu	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala
	610					615					620				
Lys	Val	Leu	Leu	Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met
	625				630					635					640
Asp	Arg	Leu	Pro	Arg	Asp	Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile
				645					650					655	
Val	Arg	Leu	Leu	Asp	Glu	Tyr	Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His
		660						665					670		
Gly	Ala	Pro	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser
		675					680					685			
Pro	Asn	Gly	Tyr	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys
	690					695					700				
Val	Arg	Lys	Pro	Ser	Ser	Lys	Gly	Leu	Ala	Cys	Gly	Ser	Lys	Glu	Ala
	705					710					715				720
Lys	Asp	Leu	Lys	Ala	Arg	Arg	Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys
				725					730					735	

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Leu Leu Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser  
740 745 750

Pro His Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser  
755 760 765

Pro Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met  
770 775 780

Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro  
785 790 795 800

Glu Met Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly  
805 810 815

Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val  
820 825 830

Leu Gly Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser  
835 840 845

Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly  
850 855 860

Met Val Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly  
865 870 875 880

Pro Leu Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro  
885 890 895

Leu His Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr  
900 905 910

Gln Gly Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln  
915 920 925

Thr Gln Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu  
930 935 940

Gln Pro Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro  
945 950 955 960

Pro Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu  
965 970 975

Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro  
980 985 990

Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser  
995 1000 1005

Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr  
1010 1015 1020

Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro  
1025 1030 1035 1040

Val Asp Asn Thr Pro Ser His Gln Leu Gln Val Pro Val Pro Val Met  
1045 1050 1055

Val Met Ile Arg Ser Ser Asp Pro Ser Lys Gly Ser Ser Ile Leu Ile  
1060 1065 1070

Glu Ala Pro Asp Ser Trp  
1075

(2) INFORMATION FOR SEQ ID NO:12:

112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4268 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..1972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC 46  
 Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys  
 1 5 10 15

ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT 94  
 Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser  
 20 25 30

GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC 142  
 Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp  
 35 40 45

TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT 190  
 Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly  
 50 55 60

GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC 238  
 Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala  
 65 70 75

AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG 286  
 Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met  
 80 85 90 95

GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC 334  
 Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val  
 100 105 110

TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG 382  
 Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met  
 115 120 125

AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG 430  
 Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu  
 130 135 140

GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG 478  
 Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val  
 145 150 155

GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT 526  
 Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn  
 160 165 170 175

GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG 574  
 Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met  
 180 185 190

CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG 622  
 Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly  
 195 200 205

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AGC	TAT	GAA	GCA	GCC	AAG	ATC	CTG	TTA	GAC	CAT	TTT	GCC	AAT	CGA	GAC	670
Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	Asp	His	Phe	Ala	Asn	Arg	Asp	
		210					215					220				
ATC	ACA	GAC	CAT	ATG	GAT	CGT	CTT	CCC	CGG	GAT	GTG	GCT	CGG	GAT	CGC	718
Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp	Val	Ala	Arg	Asp	Arg	
	225					230					235					
ATG	CAC	CAT	GAC	ATT	GTG	CGC	CTT	CTG	GAT	GAA	TAC	AAT	GTG	ACC	CCA	766
Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	Asp	Glu	Tyr	Asn	Val	Thr	Pro	
240					245					250					255	
AGC	CCT	CCA	GGC	ACC	GTG	TTG	ACT	TCT	GCT	CTC	TCA	CCT	GTC	ATC	TGT	814
Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Val	Ile	Cys	
				260					265					270		
GGG	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTG	AAG	CAC	ACC	CCA	ATG	GGC	AAG	862
Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His	Thr	Pro		Gly	Lys	
			275					280				285				
AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	ACC	ATG	CCT	ACT	AGC	CTC	CCT	910
Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met	Pro	Thr	Ser	Leu	Pro	
		290					295					300				
AAC	CTT	GCC	AAG	GAG	GCA	AAG	GAT	GCC	AAG	GGT	AGT	AGG	AGG	AAG	AAG	958
Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly	Ser	Arg	Arg	Lys	Lys	
	305					310					315					
TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	GAG	AGT	TCA	GTA	ACT	TTA	TCC	1006
Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	Glu	Ser	Ser	Val	Thr	Leu	Ser	
320					325					330					335	
CCT	GTT	GAT	TCC	CTA	GAA	TCT	CCT	CAC	ACG	TAT	GTT	TCC	GAC	ACC	ACA	1054
Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr	Val	Ser	Asp	Thr	Thr	
				340					345					350		
TCC	TCT	CCA	ATG	ATT	ACA	TCC	CCT	GGG	ATC	TTA	CAG	GCC	TCA	CCC	AAC	1102
Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu	Gln	Ala	Ser	Pro	Asn	
			355					360				365				
CCT	ATG	TTG	GCC	ACT	GCC	GCC	CCT	CCT	GCC	CCA	GTC	CAT	GCC	CAG	CAT	1150
Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Gln	His	
		370					375					380				
GCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	ATG	CAG	CCT	TTG	GCA	CAT	GGG	1198
Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln	Pro	Leu	Ala	His	Gly	
	385					390					395					
GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	
400					405					410					415	
ATT	GTG	TCT	CCA	GGC	AGT	GGC	AGT	GCT	GGA	AGC	TTG	AGT	AGG	CTC	CAT	1294
Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	
				420					425					430		
CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATG	AAC	CGC	ATG	GAG	GTG	AAT	GAG	1342
Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	
			435					440				445				
ACC	CAG	TAC	AAT	GAG	ATG	TTT	GGT	ATG	GTC	CTG	GCT	CCA	GCT	GAG	GGC	1390
Thr	Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	
		450					455					460				
ACC	CAT	CCT	GGC	ATA	GCT	CCC	CAG	AGC	AGG	CCA	CCT	GAA	GGG	AAG	CAC	1438
Thr	His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	
		465				470					475					

B

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ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu 480 485 490 495	1486
ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln 500 505 510	1534
TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln 515 520 525	1582
ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met 530 535 540	1630
ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser 580 585 590	1774
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser 595 600 605	1822
CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAGA TGTTCTTATT CAGATAATGC AAGAGAAGCA ATTCGTCAGT	2142
TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA	2202
ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTACTCTC TTCTATTTGG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCCTG TTGGAATTA TGCCCTGGAA	2382
TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCAATTGG	2442
TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC	2502
CTTTGTGCTT TTGATCATTG TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC	2622

B

115

TTTCAAGTAT GTTGTCTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT 2682  
 CATTCTGGA GAGAGAAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742  
 ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802  
 TTACCAGGAA GAAGGTGTG AGTTTGTGT TTTTCTGTGT ATGGGCCTGG TCAGTGATAA 2862  
 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922  
 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982  
 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042  
 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102  
 AACTGTTGAG CCTTTCCTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCCTG 3162  
 CCATTTAGGA CTGAACCTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222  
 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282  
 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342  
 TTATATGTTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402  
 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462  
 TTCTTTTCTT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522  
 AACATTTTCC TTTCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582  
 TTGTTTCTGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642  
 TCTTTGACTT TCTTTTAAAG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT 3702  
 CTTCTCTTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC 3762  
 AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTCTGCT CTGGGCATTT TGTAGATATT 3822  
 AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCTT CTATGGCTGC 3882  
 AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC 3942  
 CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT 4002  
 TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC 4062  
 TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT 4122  
 TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA 4182  
 ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG 4242  
 GCGATGGCGA TGACTTTCTT CCCCTG 4268

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 657 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

116

Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr  
 1 5 10 15  
 Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp  
 20 25 30  
 Glu Asp Glu Asp Ala Glu Asp Ser Ala Asn Ile Ile Thr Asp Leu  
 35 40 45  
 Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu  
 50 55 60  
 Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys  
 65 70 75 80  
 Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly  
 85 90 95  
 Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe  
 100 105 110  
 Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn  
 115 120 125  
 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly  
 130 135 140  
 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp  
 145 150 155 160  
 Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Val Asn Asn Val  
 165 170 175  
 Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln  
 180 185 190  
 Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser  
 195 200 205  
 Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp Ile  
 210 215 220  
 Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg Met  
 225 230 235 240  
 His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro Ser  
 245 250 255  
 Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys Gly  
 260 265 270  
 Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys Lys  
 275 280 285  
 Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro Asn  
 290 295 300  
 Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys Ser  
 305 310 315 320  
 Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser Pro  
 325 330 335  
 Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr Ser  
 340 345 350  
 Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn Pro

B

117



355					360					365					
Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Gln	His	Ala
	370					375					380				
Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Gln	Pro	Leu	Ala	His	Gly	Ala
385					390					395					400
Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	Ile
				405					410					415	
Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	Pro
			420					425					430		
Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	Thr
		435					440					445			
Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	Thr
	450					455					460				
His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	Ile
465					470					475					480
Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Gln	Leu	Ile
				485					490					495	
Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly	Ala	Pro	Gln	Pro	Gln	Ser
			500					505					510		
Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Gln	Ile
		515					520					525			
Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	Met
	530					535					540				
Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr	Ile	Leu	Pro	Ala	Tyr	His
545					550					555					560
Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr	Pro	Thr	Pro	Pro	Ser	Gln	His
				565					570					575	
Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala	Glu	Arg	Thr	Pro	Ser	His	Ser	Gly
			580					585					590		
His	Leu	Gln	Gly	Glu	His	Pro	Tyr	Leu	Thr	Pro	Ser	Pro	Glu	Ser	Pro
		595					600					605			
Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Ala	Ser	Asp	Trp	Ser	Asp
	610					615					620				
Val	Thr	Thr	Ser	Pro	Thr	Pro	Gly	Gly	Ala	Gly	Gly	Gly	Gln	Arg	Gly
625					630					635					640
Pro	Gly	Thr	His	Met	Ser	Glu	Pro	Pro	His	Asn	Asn	Met	Gln	Val	Tyr
				645					650					655	

Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asp Ile Asp Glu Cys Asp Gln Gly Ser Pro Cys Glu His Asn Gly  
1 5 10 15  
Ile Cys Val Asn Thr Pro Gly Ser Tyr Arg Cys Asn Cys Ser Gln Gly  
20 25 30  
Phe Thr Gly Pro Arg Cys Glu Thr Asn Ile Asn Glu Cys Glu Ser His  
35 40 45  
Pro Cys Gln Asn Glu Gly Ser Cys Leu Asp Asp Pro Gly Thr Phe Arg  
50 55 60  
Cys Val Cys Met Pro Gly Phe Thr Gly Thr Gln Cys Glu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Asp Val Asp Glu Cys Ser Leu Gly Ala Asn Pro Cys Glu His Gly  
1 5 10 15  
Gly Arg Cys Thr Asn Thr Leu Gly Ser Phe Gln Cys Asn Cys Pro Gln  
20 25 30  
Gly Tyr Ala Gly Pro Arg Cys Glu Ile Asp Val Asn Glu Cys Leu Ser  
35 40 45  
Asn Pro Cys Gln Asn Asp Ser Thr Cys Leu Asp Gln Ile Gly Glu Phe  
50 55 60  
Gln Cys Ile Cys Met Pro Gly Tyr Glu Gly Leu Tyr Cys Glu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 654 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Pro Pro Gln Gly Glu Ile Glu Ala Asp Cys Met Asp Val Asn Val

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1	5	10	15
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly	20	25	30
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Ser Ala	35	40	45
Asn Met Ile Ser Asp Phe Ile Gly Gln Gly Ala Gln Leu His Asn Gln	50	55	60
Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ala	65	70	75
Arg Ala Asp Ala Ala Lys Arg Leu Leu Glu Ser Ser Ala Asp Ala Asn	85	90	95
Val Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ala Ala	100	105	110
Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp	115	120	125
Leu Asp Ala Arg Met Phe Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala	130	135	140
Arg Leu Ala Val Glu Gly Met Val Glu Glu Leu Ile Asn Ala His Ala	145	150	155
Asp Val Asn Ala Val Asp Glu Phe Gly Lys Ser Ala Leu His Trp Ala	165	170	175
Ala Ala Val Asn Asn Val Asp Ala Ala Ala Val Leu Leu Lys Asn Ser	180	185	190
Ala Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Ser Leu Phe Leu	195	200	205
Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His	210	215	220
Tyr Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp	225	230	235
Ile Ala Gln Glu Arg Met His His Asp Ile Val His Leu Leu Asp Glu	245	250	255
Tyr Asn Leu Val Lys Ser Pro Thr Leu His Asn Gly Pro Leu Gly Ala	260	265	270
Thr Thr Leu Ser Pro Pro Ile Cys Ser Pro Asn Gly Tyr Met Gly Asn	275	280	285
Met Lys Pro Ser Val Gln Ser Lys Lys Ala Arg Lys Pro Ser Ile Lys	290	295	300
Gly Asn Gly Cys Lys Glu Ala Lys Glu Leu Lys Ala Arg Arg Lys Lys	305	310	315
Ser Gln Asp Gly Lys Thr Thr Leu Leu Asp Ser Gly Ser Ser Gly Val	325	330	335
Leu Ser Pro Val Asp Ser Leu Glu Ser Thr His Gly Tyr Leu Ser Asp	340	345	350
Val Ser Ser Pro Pro Leu Met Thr Ser Pro Phe Gln Gln Ser Pro Ser	355	360	365

B

120

Met Pro Leu Asn His Leu Thr Ser Met Pro Glu Ser Gln Leu Gly Met  
370 375 380

Asn His Ile Asn Met Ala Thr Lys Gln Glu Met Ala Ala Gly Ser Asn  
385 390 395 400

Arg Met Ala Phe Asp Ala Met Val Pro Arg Leu Thr His Leu Asn Ala  
405 410 415

Ser Ser Pro Asn Thr Ile Met Ser Asn Gly Ser Met His Phe Thr Val  
420 425 430

Gly Gly Ala Pro Thr Met Asn Ser Gln Cys Asp Trp Leu Ala Arg Leu  
435 440 445

Gln Asn Gly Met Val Gln Asn Gln Tyr Asp Pro Ile Arg Asn Gly Ile  
450 455 460

Gln Gln Gly Asn Ala Gln Gln Ala Gln Ala Leu Gln His Gly Leu Met  
465 470 475 480

Thr Ser Leu His Asn Gly Leu Pro Ala Thr Thr Leu Ser Gln Met Met  
485 490 495

Thr Tyr Gln Ala Met Pro Asn Thr Arg Leu Ala Asn Gln Pro His Leu  
500 505 510

Met Gln Ala Gln Gln Met Gln Gln Gln Gln Asn Leu Gln Leu His Gln  
515 520 525

Ser Met Gln Gln Gln His His Asn Ser Ser Thr Thr Ser Thr His Ile  
530 535 540

Asn Ser Pro Phe Cys Ser Ser Asp Ile Ser Gln Thr Asp Leu Gln Gln  
545 550 555 560

Met Ser Ser Asn Asn Ile His Ser Val Met Pro Gln Asp Thr Gln Ile  
565 570 575

Phe Ala Ala Ser Leu Pro Ser Asn Leu Thr Gln Ser Met Thr Thr Ala  
580 585 590

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Met Asp  
595 600 605

Asn Thr Pro Ser His Gln Leu Gln Val Pro Asp His Pro Phe Leu Thr  
610 615 620

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser  
625 630 635 640

Asn Met Ser Asp Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr  
645 650

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

121

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val  
 1 5 10 15  
 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly  
 20 25 30  
 Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala  
 35 40 45  
 Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr  
 50 55 60  
 Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg  
 65 70 75 80  
 Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile  
 85 90 95  
 Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp  
 100 105 110  
 Ala Gln Gly Val Phe Gln Ile Leu Leu Arg Asn Arg Ala Thr Asp Leu  
 115 120 125  
 Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg  
 130 135 140  
 Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp  
 145 150 155 160  
 Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala  
 165 170 175  
 Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala  
 180 185 190  
 Asn Lys Asp Met Gln Asn Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala  
 195 200 205  
 Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe  
 210 215 220  
 Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile  
 225 230 235 240  
 Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr  
 245 250 255  
 Asn Leu Val Arg Ser Pro Gln Leu His Gly Thr Ala Leu Gly Gly Thr  
 260 265 270  
 Pro Thr Leu Ser Pro Thr Leu Cys Ser Pro Asn Gly Tyr Leu Gly Asn  
 275 280 285  
 Leu Lys Ser Ala Thr Gln Gly Lys Lys Ala Arg Lys Pro Ser Thr Lys  
 290 295 300  
 Gly Leu Ala Cys Ser Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg  
 305 310 315 320  
 Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Ser Met  
 325 330 335  
 Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Gly Tyr Leu Ser Asp  
 340 345 350  
 Val Ala Ser Pro Pro Leu Pro Ser Pro Phe Gln Gln Ser Pro Ser Met

B

122

355		360		365
Pro Leu Ser His Leu Pro Gly Met Pro Asp Thr His Leu Gly Ile Ser				
370		375		380
His Leu Asn Val Ala Ala Lys Pro Glu Met Ala Ala Leu Ala Gly Gly				
385		390		395
Ser Arg Leu Ala Phe Glu Pro Pro Pro Pro Arg Leu Ser His Leu Pro				
		405		410
Val Ala Ser Ser Ala Ser Thr Val Leu Ser Thr Asn Gly Thr Gly Ala				
		420		425
Met Asn Phe Thr Val Gly Ala Pro Ala Ser Leu Asn Gly Gln Cys Glu				
		435		440
Trp Leu Pro Arg Leu Gln Asn Gly Met Val Pro Ser Gln Tyr Asn Pro				
		450		455
Leu Arg Pro Gly Val Thr Pro Gly Thr Leu Ser Thr Gln Ala Ala Gly				
		465		470
Leu Gln His Gly Met Met Ser Pro Ile His Ser Ser Leu Ser Thr Asn				
		485		490
Thr Leu Ser Pro Ile Ile Tyr Gln Gly Leu Pro Asn Thr Arg Leu Ala				
		500		505
Thr Gln Pro His Leu Val Gln Thr Gln Gln Val Gln Pro Gln Asn Leu				
		515		520
Gln Ile Gln Pro Gln Asn Leu Gln Pro Pro Ser Gln Pro His Leu Ser				
		530		535
Val Ser Ser Ala Ala Asn Gly His Leu Gly Arg Ser Phe Leu Ser Gly				
		545		550
Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly Pro Ser Ser Leu Pro				
		565		570
Val His Thr Ile Leu Pro Gln Glu Ser Gln Ala Leu Pro Thr Ser Leu				
		580		585
Pro Ser Ser Met Val Pro Pro Met Thr Thr Thr Gln Phe Leu Thr Pro				
		595		600
Pro Ser Gln His Ser Tyr Ser Ser Ser Pro Val Asp Asn Thr Pro Ser				
		610		615
His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu				
		625		630
Ser Pro Asp Gln Trp Ser Ser Ser Ser Arg His Ser Asn Ile Ser Asp				
		645		650
Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr				
		660		665

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 681 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

123

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val  
1 5 10 15  
Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly  
20 25 30  
Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala  
35 40 45  
Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr  
50 55 60  
Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg Tyr Ser Arg  
65 70 75 80  
Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile  
85 90 95  
Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp  
100 105 110  
Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp Leu  
115 120 125  
Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg  
130 135 140  
Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile Asn Ser His Ala Asp  
145 150 155 160  
Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala  
165 170 175  
Ala Val Asn Asn Val Asp Ala Ala Val Val Leu Leu Lys Asn Gly Ala  
180 185 190  
Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr Pro Leu Phe Leu Ala  
195 200 205  
Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe  
210 215 220  
Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile  
225 230 235 240  
Ala Gln Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr  
245 250 255  
Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala Pro Leu Gly Gly Thr  
260 265 270  
Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly Tyr Leu Gly Ser  
275 280 285  
Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg Lys Pro Ser Ser Lys  
290 295 300  
Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp Leu Lys Ala Arg Arg  
305 310 315 320  
Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp Ser Ser Gly Met

B

124

325										330					335				
Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Gly	Tyr	Leu	Ser	Asp				
			340					345					350						
Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser				
		355					360					365							
Val	Pro	Leu	Asn	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile				
	370					375					380								
Gly	His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Gly	Gly				
385					390					395					400				
Gly	Gly	Arg	Leu	Ala	Phe	Glu	Thr	Gly	Pro	Pro	Arg	Leu	Ser	His	Leu				
				405					410					415					
Pro	Val	Ala	Ser	Gly	Thr	Ser	Thr	Val	Leu	Gly	Ser	Ser	Ser	Gly	Gly				
			420					425					430						
Ala	Leu	Asn	Phe	Thr	Val	Gly	Gly	Ser	Thr	Ser	Leu	Asn	Gly	Gln	Cys				
		435					440					445							
Glu	Trp	Leu	Ser	Arg	Leu	Gln	Ser	Gly	Met	Val	Pro	Asn	Gln	Tyr	Asn				
	450					455					460								
Pro	Leu	Arg	Gly	Ser	Val	Ala	Pro	Gly	Pro	Leu	Ser	Thr	Gln	Ala	Pro				
465					470					475					480				
Ser	Leu	Gln	His	Gly	Met	Val	Gly	Pro	Leu	His	Ser	Ser	Leu	Ala	Ala				
				485					490					495					
Ser	Ala	Leu	Ser	Gln	Met	Met	Ser	Tyr	Gln	Gly	Leu	Pro	Ser	Thr	Arg				
			500					505					510						
Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln				
		515					520					525							
Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu	Gln	Pro	Ala	Asn	Ile	Gln	Gln				
	530					535					540								
Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Pro	His	Leu	Gly				
545					550					555					560				
Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu	Gly	Arg	Ser	Phe	Leu	Ser	Gly				
			565						570					575					
Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Gly	Pro	Ser	Ser	Leu	Ala				
			580					585					590						
Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Pro	Ala	Leu	Pro	Thr	Ser	Leu				
		595					600					605							
Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	Ala	Ala	Gln	Phe	Leu	Thr	Pro				
	610					615					620								
Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	Val	Glu	Asn	Thr	Pro	Ser	His				
625					630					635					640				
Gln	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu	Ser				
			645						650					655					
Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Asn	Val	Ser	Asp	Trp				
			660					665					670						
Ser	Glu	Gly	Val	Ser	Ser	Pro	Pro	Thr											
		675					680												

B

125



(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp  
1 5 10 15

Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly Tyr  
20 25 30

Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn Gly Thr  
35 40 45

Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His  
50 55 60

Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val  
65 70 75 80

Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe  
85 90 95

Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser  
100 105 110

Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg Asp Thr  
115 120 125

Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys Gln Trp  
130 135 140

Thr Asp Ala Cys Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr  
145 150 155 160

Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly  
165 170 175

Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys  
180 185 190

Gln His Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln  
195 200 205

Cys Pro Gln Gly Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro  
210 215 220

Cys Ala Pro Ser Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly  
225 230 235 240

Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Gly Phe Glu Gly Ser Thr  
245 250 255

Cys Glu Arg Asn Ile Asp Asp Cys Pro Asn His Arg Cys Gln Asn Gly  
260 265 270

Gly Val Cys Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro  
275 280 285

B

126

Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp Glu Cys Leu Leu  
290 295 300

Gln Pro Asn Ala Cys Gln Asn Gly Gly Thr Cys Ala Asn Arg Asn Gly  
305 310 315 320

Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser Gly Asp Asp Cys Ser  
325 330 335

Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys Thr Pro Gly Ser Thr  
340 345 350

Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met Cys Pro Glu Gly Lys  
355 360 365

Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys Ile Ser Asn Pro Cys  
370 375 380

His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile  
385 390 395 400

Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val  
405 410 415

Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys  
420 425 430

Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr  
435 440 445

Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro  
450 455 460

Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys  
465 470 475 480

Leu Cys Met Pro Gly Phe Lys Gly Val His Cys Glu Leu Glu Ile Asn  
485 490 495

Glu Cys Gln Ser Asn Pro Cys Val Asn Asn Gly Gln Cys Val Asp Lys  
500 505 510

Val Asn Arg Phe Gln Cys Leu Cys Pro Pro Gly Phe Thr Gly Pro Val  
515 520 525

Cys Gln Ile Asp Ile Asp Asp Cys Ser Ser Thr Pro Cys Leu Asn Gly  
530 535 540

Ala Lys Cys Ile Asp His Pro Asn Gly Tyr Glu Cys Gln Cys Ala Thr  
545 550 555 560

Gly Phe Thr Gly Val Leu Cys Glu Glu Asn Ile Asp Asn Cys Asp Pro  
565 570 575

Asp Pro Cys His His Gly Gln Cys Gln Asp Gly Ile Asp Ser Tyr Thr  
580 585 590

Cys Ile Cys Asn Pro Gly Tyr Met Gly Ala Ile Cys Ser Asp Gln Ile  
595 600 605

Asp Glu Cys Tyr Ser Ser Pro Cys Leu Asn Asp Gly Arg Cys Ile Asp  
610 615 620

Leu Val Asn Gly Tyr Gln Cys Asn Cys Gln Pro Gly Thr Ser Gly Val  
625 630 635 640

Asn Cys Glu Ile Asn Phe Asp Asp Cys Ala Ser Asn Pro Cys Ile His

B



B

128

Phe Ser Cys Leu Cys Pro Val Gly Phe Thr Gly Ser Phe Cys Leu His  
 1010 1015 1020  
 Glu Ile Asn Glu Cys Ser Ser His Pro Cys Leu Asn Glu Gly Thr Cys  
 1025 1030 1035 1040  
 Val Asp Gly Leu Gly Thr Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr  
 1045 1050 1055  
 Gly Lys Asn Cys Gln Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys  
 1060 1065 1070  
 Lys Asn Lys Gly Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu  
 1075 1080 1085  
 Cys Pro Ser Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser  
 1090 1095 1100  
 Cys Asp Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys  
 1105 1110 1115 1120  
 Gln His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys Gln  
 1125 1130 1135  
 Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu Asp Glu  
 1140 1145 1150  
 Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser Asp Phe Ile  
 1155 1160 1165  
 Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val Asn Cys  
 1170 1175 1180  
 Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn Gly Gly  
 1185 1190 1195 1200  
 Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro Pro Gly  
 1205 1210 1215  
 Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala Arg Gly  
 1220 1225 1230  
 Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly Gly Tyr  
 1235 1240 1245  
 Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu Gly Asp  
 1250 1255 1260  
 Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser Leu Asp  
 1265 1270 1275 1280  
 Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe  
 1285 1290 1295  
 Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro  
 1300 1305 1310  
 Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly  
 1315 1320 1325  
 Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser  
 1330 1335 1340  
 Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr  
 1345 1350 1355 1360  
 Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu Ser

1365										1370					1375				
Gly	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	Pro	Gln				
			1380					1385					1390						
Arg	Gln	Pro	Pro	Tyr	Tyr	Ser	Cys	Gln	Cys	Ala	Pro	Pro	Phe	Ser	Gly				
		1395					1400						1405						
Ser	Arg	Cys	Glu	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Thr	Pro	Pro	Ala	Thr				
	1410					1415					1420								
Cys	Leu	Ser	Gln	Tyr	Cys	Ala	Asp	Lys	Ala	Arg	Asp	Gly	Val	Cys	Asp				
1425					1430					1435					1440				
Glu	Ala	Cys	Asn	Ser	His	Ala	Cys	Gln	Trp	Asp	Gly	Gly	Asp	Cys	Ser				
			1445						1450					1455					
Leu	Thr	Met	Glu	Asn	Pro	Trp	Ala	Asn	Cys	Ser	Ser	Pro	Leu	Pro	Cys				
			1460					1465					1470						
Trp	Asp	Tyr	Ile	Asn	Asn	Gln	Cys	Asp	Glu	Leu	Cys	Asn	Thr	Val	Glu				
	1475						1480						1485						
Cys	Leu	Phe	Asp	Asn	Phe	Glu	Cys	Gln	Gly	Asn	Ser	Lys	Thr	Cys	Lys				
	1490					1495					1500								
Tyr	Asp	Lys	Tyr	Cys	Ala	Asp	His	Phe	Lys	Asp	Asn	His	Cys	Asn	Gln				
1505					1510					1515					1520				
Gly	Cys	Asn	Ser	Glu	Glu	Cys	Gly	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Ala				
				1525					1530					1535					
Asp	Gln	Pro	Glu	Asn	Leu	Ala	Glu	Gly	Thr	Leu	Val	Ile	Val	Val	Leu				
			1540					1545					1550						
Met	Pro	Pro	Glu	Gln	Leu	Leu	Gln	Asp	Ala	Arg	Ser	Phe	Leu	Arg	Ala				
			1555				1560					1565							
Leu	Gly	Thr	Leu	Leu	His	Thr	Asn	Leu	Arg	Ile	Lys	Arg	Asp	Ser	Gln				
	1570					1575					1580								
Gly	Glu	Leu	Met	Val	Tyr	Pro	Tyr	Tyr	Gly	Glu	Lys	Ser	Ala	Ala	Met				
1585					1590					1595					1600				
Lys	Lys	Gln	Arg	Met	Thr	Arg	Arg	Ser	Leu	Pro	Gly	Glu	Gln	Glu	Gln				
				1605					1610				1615						
Glu	Val	Ala	Gly	Ser	Lys	Val	Phe	Leu	Glu	Ile	Asp	Asn	Arg	Gln	Cys				
			1620					1625					1630						
Val	Gln	Asp	Ser	Asp	His	Cys	Phe	Lys	Asn	Thr	Asp	Ala	Ala	Ala	Ala				
			1635				1640					1645							
Leu	Leu	Ala	Ser	His	Ala	Ile	Gln	Gly	Thr	Leu	Ser	Tyr	Pro	Leu	Val				
	1650					1655					1660								
Ser	Val	Val	Ser	Glu	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Gln	Leu	Leu	Tyr				
1665					1670					1675					1680				
Leu	Leu	Ala	Val	Ala	Val	Val	Ile	Ile	Leu	Phe	Ile	Ile	Leu	Leu	Gly				
				1685					1690					1695					
Val	Ile	Met	Ala	Lys	Arg	Lys	Arg	Lys	His	Gly	Ser	Leu	Trp	Leu	Pro				
			1700				1705						1710						
Glu	Gly	Phe	Thr	Leu	Arg	Arg	Asp	Ala	Ser	Asn	His	Lys	Arg	Arg	Glu				
			1715				1720					1725							

B

130

Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val Gln Val  
1730 1735 1740

Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp Val Asp  
1745 1750 1755 1760

Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu Ala Leu  
1765 1770 1775

Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr Gln Gln  
1780 1785 1790

His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala Leu Thr  
1795 1800 1805

Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg  
1810 1815 1820

Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly  
1825 1830 1835 1840

Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala  
1845 1850 1855

Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln  
1860 1865 1870

Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser  
1875 1880 1885

Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn  
1890 1895 1900

Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala  
1905 1910 1915 1920

Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp  
1925 1930 1935

Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala  
1940 1945 1950

Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala  
1955 1960 1965

Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His Trp Ala  
1970 1975 1980

Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly  
1985 1990 1995 2000

Ala Asn Arg Asp Met Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu  
2005 2010 2015

Ala Ala Arg Glu Gly Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His  
2020 2025 2030

Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp  
2035 2040 2045

Val Ala Arg Asp Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu  
2050 2055 2060

Tyr Asn Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu  
2065 2070 2075 2080

Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His

B

131

2085	2090	2095
Thr Pro Met Gly Lys Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met 2100	2105	2110
Pro Thr Ser Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly 2115	2120	2125
Ser Arg Arg Lys Lys Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser 2130	2135	2140
Ser Val Thr Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr 2145	2150	2155
Val Ser Asp Thr Thr Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu 2165	2170	2175
Gln Ala Ser Pro Asn Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro 2180	2185	2190
Val His Ala Gln His Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln 2195	2200	2205
Pro Leu Ala His Gly Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu 2210	2215	2220
Leu Ser His His His Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser 2225	2230	2235
Leu Ser Arg Leu His Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg 2245	2250	2255
Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu 2260	2265	2270
Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro 2275	2280	2285
Pro Glu Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile 2290	2295	2300
Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly 2305	2310	2315
Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu 2325	2330	2335
Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala 2340	2345	2350
Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr 2355	2360	2365
Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro 2370	2375	2380
Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg 2385	2390	2395
Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr 2405	2410	2415
Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser 2420	2425	2430
Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala 2435	2440	2445

Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro Pro His  
2450 2455 2460

Asn Asn Met Gln Val Tyr Ala  
2465 2470

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2556 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala  
1 5 10 15  
Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu  
20 25 30  
Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys  
35 40 45  
Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu  
50 55 60  
Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg  
65 70 75 80  
Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro  
85 90 95  
Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg  
100 105 110  
Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg  
115 120 125  
Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys  
130 135 140  
Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala  
145 150 155 160  
Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg  
165 170 175  
Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly  
180 185 190  
Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala  
195 200 205  
Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro  
210 215 220  
Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr  
225 230 235 240  
His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu  
245 250 255

B

133



Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys  
 260 265 270  
 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr  
 275 280 285  
 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn  
 290 295 300  
 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn  
 305 310 315 320  
 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile  
 325 330 335  
 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp  
 340 345 350  
 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu  
 355 360 365  
 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly  
 370 375 380  
 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys  
 385 390 395 400  
 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys  
 405 410 415  
 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr  
 420 425 430  
 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg  
 435 440 445  
 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp  
 450 455 460  
 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro  
 465 470 475 480  
 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser  
 485 490 495  
 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe  
 500 505 510  
 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp  
 515 520 525  
 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu  
 530 535 540  
 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly  
 545 550 555 560  
 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His  
 565 570 575  
 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg  
 580 585 590  
 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser  
 595 600 605  
 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala

B

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610					615					620					
Tyr 625	Leu	Cys	Phe	Cys	Leu 630	Lys	Gly	Thr	Thr	Gly 635	Pro	Asn	Cys	Glu	Ile 640
Asn	Leu	Asp	Asp	Cys 645	Ala	Ser	Ser	Pro	Cys 650	Asp	Ser	Gly	Thr	Cys 655	Leu
Asp	Lys	Ile	Asp 660	Gly	Tyr	Glu	Cys	Ala 665	Cys	Glu	Pro	Gly	Tyr 670	Thr	Gly
Ser	Met	Cys 675	Asn	Ser	Asn	Ile	Asp 680	Glu	Cys	Ala	Gly	Asn 685	Pro	Cys	His
Asn	Gly 690	Gly	Thr	Cys	Glu	Asp 695	Gly	Ile	Asn	Gly	Phe 700	Thr	Cys	Arg	Cys
Pro 705	Glu	Gly	Tyr	His	Asp 710	Pro	Thr	Cys	Leu	Ser 715	Glu	Val	Asn	Glu	Cys 720
Asn	Ser	Asn	Pro	Cys 725	Val	His	Gly	Ala	Cys 730	Arg	Asp	Ser	Leu	Asn	Gly 735
Tyr	Lys	Cys	Asp 740	Cys	Asp	Pro	Gly	Trp 745	Ser	Gly	Thr	Asn	Cys 750	Asp	Ile
Asn	Asn	Asn	Glu	Cys	Glu	Ser	Asn 760	Pro	Cys	Val	Asn	Gly 765	Gly	Thr	Cys
Lys	Asp 770	Met	Thr	Ser	Gly	Ile 775	Val	Cys	Thr	Cys	Arg 780	Glu	Gly	Phe	Ser
Gly 785	Pro	Asn	Cys	Gln	Thr 790	Asn	Ile	Asn	Glu	Cys 795	Ala	Ser	Asn	Pro	Cys 800
Leu	Asn	Lys	Gly	Thr 805	Cys	Ile	Asp	Asp	Val 810	Ala	Gly	Tyr	Lys	Cys 815	Asn
Cys	Leu	Leu	Pro 820	Tyr	Thr	Gly	Ala	Thr 825	Cys	Glu	Val	Val	Leu	Ala	Pro
Cys	Ala	Pro 835	Ser	Pro	Cys	Arg	Asn 840	Gly	Gly	Glu	Cys	Arg 845	Gln	Ser	Glu
Asp	Tyr 850	Glu	Ser	Phe	Ser	Cys 855	Val	Cys	Pro	Thr	Ala 860	Gly	Ala	Lys	Gly
Gln	Thr	Cys	Glu	Val	Asp 870	Ile	Asn	Glu	Cys	Val 875	Leu	Ser	Pro	Cys	Arg 880
His	Gly	Ala	Ser	Cys 885	Gln	Asn	Thr	His	Gly 890	Gly	Tyr	Arg	Cys	His 895	Cys
Gln	Ala	Gly	Tyr 900	Ser	Gly	Arg	Asn	Cys 905	Glu	Thr	Asp	Ile	Asp 910	Asp	Cys
Arg	Pro	Asn 915	Pro	Cys	His	Asn	Gly 920	Gly	Ser	Cys	Thr	Asp 925	Gly	Ile	Asn
Thr	Ala 930	Phe	Cys	Asp	Cys	Leu 935	Pro	Gly	Phe	Arg	Gly 940	Thr	Phe	Cys	Glu
Glu	Asp	Ile	Asn	Glu	Cys 950	Ala	Ser	Asp	Pro	Cys 955	Arg	Asn	Gly	Ala	Asn 960
Cys	Thr	Asp	Cys	Val 965	Asp	Ser	Tyr	Thr	Cys 970	Thr	Cys	Pro	Ala	Gly 975	Phe

B

135

Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser  
980 985 990

Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys  
995 1000 1005

Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn  
1010 1015 1020

Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly  
1025 1030 1035 1040

Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn  
1045 1050 1055

Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly  
1060 1065 1070

Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser  
1075 1080 1085

Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val  
1090 1095 1100

Ala Ala Gln Arg Gln Gly Val Asp Val Ala Arg Leu Cys Gln His Gly  
1105 1110 1115 1120

Gly Leu Cys Val Asp Ala Gly Asn Thr His His Cys Arg Cys Gln Ala  
1125 1130 1135

Gly Tyr Thr Gly Ser Tyr Cys Glu Asp Leu Val Asp Glu Cys Ser Pro  
1140 1145 1150

Ser Pro Cys Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr  
1155 1160 1165

Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu  
1170 1175 1180

Ile Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu  
1185 1190 1195 1200

Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly  
1205 1210 1215

Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro  
1220 1225 1230

Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln  
1235 1240 1245

Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg  
1250 1255 1260

Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg  
1265 1270 1275 1280

Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys  
1285 1290 1295

Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys  
1300 1305 1310

Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn  
1315 1320 1325

Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala

B

136

1330	1335	1340
Thr Cys Glu Asn Asp 1345	Ala Arg Thr Cys Gly 1350	Ser Leu Arg Cys Leu Asn 1355 1360
Gly Gly Thr Cys Ile 1365	Ser Gly Pro Arg 1370	Thr Cys Leu Cys Leu 1375
Gly Pro Phe Thr 1380	Gly Pro Glu Cys Gln Phe 1385	Pro Ala Ser Ser Pro Cys 1390
Leu Gly Gly Asn Pro Cys Tyr 1395	Asn Gln Gly Thr Cys 1400	Glu Pro Thr Ser 1405
Glu Ser Pro Phe Tyr Arg 1410	Cys Leu Cys Pro Ala Lys 1415 1420	Phe Asn Gly Leu
Leu Cys His Ile Leu Asp Tyr Ser Phe 1425	Gly Gly Gly Ala Gly Arg 1430 1435	Asp 1440
Ile Pro Pro Pro Leu Ile Glu Glu Ala Cys Glu Leu Pro Glu Cys Gln 1445	1450	1455
Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn His Ala 1460	1465	1470
Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp Pro Trp 1475	1480	1485
Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser Asp Gly 1490	1495	1500
His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp Gly Phe 1505	1510	1515 1520
Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp Gln Tyr 1525	1530	1535
Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys Asn Ser 1540	1545	1550
Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val Pro Glu 1555	1560	1565
Arg Leu Ala Ala Gly Thr Leu Val Val Val Val Leu Met Pro Pro Glu 1570	1575	1580
Gln Leu Arg Asn Ser Ser Phe His Phe Leu Arg Glu Leu Ser Arg Val 1585	1590	1595 1600
Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln Gln Met 1605	1610	1615
Ile Phe Pro Tyr Tyr Gly Arg Glu Glu Glu Leu Arg Lys His Pro Ile 1620	1625	1630
Lys Arg Ala Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu Gly Gln 1635	1640	1645
Val Lys Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg Arg Arg 1650	1655	1660
Arg Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr Leu Glu 1665	1670	1675 1680
Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe Gln Ser 1685	1690	1695

B

137

Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu Gly Ser  
1700 1705 1710

Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr Val Glu  
1715 1720 1725

Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala Ala Ala  
1730 1735 1740

Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys  
1745 1750 1755 1760

Arg Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe Lys Val  
1765 1770 1775

Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Glu Leu Gly Glu Asp Ser  
1780 1785 1790

Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu Met Asp  
1795 1800 1805

Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe  
1810 1815 1820

Arg Phe Glu Glu Pro Val Val Leu Pro Asp Leu Asp Asp Gln Thr Asp  
1825 1830 1835 1840

His Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu Arg Met  
1845 1850 1855

Ser Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys  
1860 1865 1870

Met Asp Val Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile  
1875 1880 1885

Ala Ser Cys Ser Gly Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu  
1890 1895 1900

Glu Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser  
1905 1910 1915 1920

Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala  
1925 1930 1935

Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser  
1940 1945 1950

Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala  
1955 1960 1965

Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn  
1970 1975 1980

Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr Pro Leu  
1985 1990 1995 2000

Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu Asp Leu Ile  
2005 2010 2015

Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu Gly Lys Ser Ala  
2020 2025 2030

Leu His Trp Ala Ala Ala Val Asn Asn Val Asp Ala Ala Val Val Leu  
2035 2040 2045

Leu Lys Asn Gly Ala Asn Lys Asp Met Gln Asn Asn Arg Glu Glu Thr

B

138

2050	2055	2060
Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Thr Ala Lys Val 2065	2070	2075 2080
Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg 2085	2090	2095
Leu Pro Arg Asp Ile Ala Gln Glu Arg Met His His Asp Ile Val Arg 2100	2105	2110
Leu Leu Asp Glu Tyr Asn Leu Val Arg Ser Pro Gln Leu His Gly Ala 2115	2120	2125
Pro Leu Gly Gly Thr Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn 2130	2135	2140
Gly Tyr Leu Gly Ser Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg 2145	2150	2155 2160
Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp 2165	2170	2175
Leu Lys Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu 2180	2185	2190
Asp Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His 2195	2200	2205
Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser Pro Phe 2210	2215	2220
Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met Pro Asp 2225	2230	2235 2240
Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys Pro Glu Met 2245	2250	2255
Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu Thr Gly Pro Pro 2260	2265	2270
Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val Leu Gly 2275	2280	2285
Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr Val Gly Gly Ser Thr Ser 2290	2295	2300
Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly Met Val 2305	2310	2315 2320
Pro Asn Gln Tyr Asn Pro Leu Arg Gly Ser Val Ala Pro Gly Pro Leu 2325	2330	2335
Ser Thr Gln Ala Pro Ser Leu Gln His Gly Met Val Gly Pro Leu His 2340	2345	2350
Ser Ser Leu Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr Gln Gly 2355	2360	2365
Leu Pro Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln 2370	2375	2380
Gln Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro 2385	2390	2395 2400
Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro Pro Pro 2405	2410	2415

B

139

Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu Gly Arg  
2420 2425 2430

Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly  
2435 2440 2445

Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln Glu Ser Pro Ala  
2450 2455 2460

Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr Ala Ala  
2465 2470 2475 2480

Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Val Glu  
2485 2490 2495

Asn Thr Pro Ser His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr  
2500 2505 2510

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser  
2515 2520 2525

Asn Val Ser Asp Trp Ser Glu Gly Val Ser Ser Pro Pro Thr Ser Met  
2530 2535 2540

Gln Ser Gln Ile Ala Arg Ile Pro Glu Ala Phe Lys  
2545 2550 2555

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 10..7419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCG CCC GCC CTG CGC CCC GCT CTG CTG TGG GCG CTG CTG GCG	48
Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala	
1 5 10	
CTC TGG CTG TGC TGC GCG GCC CCC GCG CAT GCA TTG CAG TGT CGA GAT	96
Leu Trp Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp	
15 20 25	
GGC TAT GAA CCC TGT GTA AAT GAA GGA ATG TGT GTT ACC TAC CAC AAT	144
Gly Tyr Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn	
30 35 40 45	
GGC ACA GGA TAC TGC AAA TGT CCA GAA GGC TTC TTG GGG GAA TAT TGT	192
Gly Thr Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys	
50 55 60	
CAA CAT CGA GAC CCC TGT GAG AAG AAC CGC TGC CAG AAT GGT GGG ACT	240
Gln His Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr	
65 70 75	
TGT GTG GCC CAG GCC ATG CTG GGG AAA GCC ACG TGC CGA TGT GCC TCA	288
Cys Val Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser	

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80					85					90						
GGG Gly	TTT Phe 95	ACA Thr	GGA Gly	GAG Glu	GAC Asp	TGC Cys 100	CAG Gln	TAC Tyr	TCA Ser	ACA Thr	TCT Ser 105	CAT His	CCA Pro	TGC Cys	TTT Phe	336
GTG Val 110	TCT Ser	CGA Arg	CCC Pro	TGC Cys	CTG Leu 115	AAT Asn	GGC Gly	GGC Gly	ACA Thr	TGC Cys 120	CAT His	ATG Met	CTC Leu	AGC Ser	CGG Arg 125	384
GAT Asp	ACC Thr	TAT Tyr	GAG Glu	TGC Cys 130	ACC Thr	TGT Cys	CAA Gln	GTC Val	GGG Gly 135	TTT Phe	ACA Thr	GGT Gly	AAG Lys	GAG Glu 140	TGC Cys	432
CAA Gln	TGG Trp	ACG Thr	GAT Asp 145	GCC Ala	TGC Cys	CTG Leu	TCT Ser	CAT His 150	CCC Pro	TGT Cys	GCA Ala	AAT Asn	GGA Gly 155	AGT Ser	ACC Thr	480
TGT Cys	ACC Thr	ACT Thr 160	GTG Val	GCC Ala	AAC Asn	CAG Gln	TTC Phe 165	TCC Ser	TGC Cys	AAA Lys	TGC Cys	CTC Leu 170	ACA Thr	GGC Gly	TTC Phe	528
ACA Thr 175	GGG Gly	CAG Gln	AAA Lys	TGT Cys	GAG Glu	ACT Thr 180	GAT Asp	GTC Val	AAT Asn	GAG Glu	TGT Cys 185	GAC Asp	ATT Ile	CCA Pro	GGA Gly	576
CAC His 190	TGC Cys	CAG Gln	CAT His	GGT Gly	GGC Gly 195	ACC Thr	TGC Cys	CTC Leu	AAC Asn	CTG Leu 200	CCT Pro	GGT Gly	TCC Ser	TAC Tyr	CAG Gln 205	624
TGC Cys	CAG Gln	TGC Cys	CCT Pro	CAG Gln 210	GGC Gly	TTC Phe	ACA Thr	GGC Gly	CAG Gln 215	TAC Tyr	TGT Cys	GAC Asp	AGC Ser	CTG Leu 220	TAT Tyr	672
GTG Val	CCC Pro	TGT Cys	GCA Ala 225	CCC Pro	TCA Ser	CCT Pro	TGT Cys	GTC Val 230	AAT Asn	GGA Gly	GGC Gly	ACC Thr	TGT Cys 235	CGG Arg	CAG Gln	720
ACT Thr	GGT Gly	GAC Asp 240	TTC Phe	ACT Thr	TTT Phe	GAG Glu 245	TGC Cys	AAC Asn	TGC Cys	CTT Leu	CCA Pro	GGT Gly 250	TTT Phe	GAA Glu	GGG Gly	768
AGC Ser	ACC Thr 255	TGT Cys	GAG Glu	AGG Arg	AAT Asn	ATT Ile 260	GAT Asp	GAC Asp	TGC Cys	CCT Pro	AAC Asn 265	CAC His	AGG Arg	TGT Cys	CAG Gln	816
AAT Asn 270	GGA Gly	GGG Gly	GTT Val	TGT Cys	GTG Val 275	GAT Asp	GGG Gly	GTC Val	AAC Asn	ACT Thr 280	TAC Tyr	AAC Asn	TGC Cys	CGC Arg	TGT Cys 285	864
CCC Pro	CCA Pro	CAA Gln	TGG Trp	ACA Thr 290	GGA Gly	CAG Gln	TTC Phe	TGC Cys	ACA Thr 295	GAG Glu	GAT Asp	GTG Val	GAT Asp	GAA Glu 300	TGC Cys	912
CTG Leu	CTG Leu	CAG Gln	CCC Pro 305	AAT Asn	GCC Ala	TGT Cys	CAA Gln	AAT Asn 310	GGG Gly	GGC Gly	ACC Thr	TGT Cys	GCC Ala 315	AAC Asn	CGC Arg	960
AAT Asn	GGA Gly	GGC Gly 320	TAT Tyr	GGC Gly	TGT Cys	GTA Val	TGT Cys 325	GTC Val	AAC Asn	GGC Gly	TGG Trp	AGT Ser 330	GGA Gly	GAT Asp	GAC Asp	1008
TGC Cys	AGT Ser 335	GAG Glu	AAC Asn	ATT Ile	GAT Asp	GAT Asp 340	TGT Cys	GCC Ala	TTC Phe	GCC Ala	TCC Ser 345	TGT Cys	ACT Thr	CCA Pro	GGC Gly	1056
TCC Gly	ACC Thr	TGC Gln	ATC Trp	GAC Asp	CGT Gln	GTG Val	GCC Gln	TCC Ser	TTC Asn	TCT Gln	TGC Cys	ATG Met	TGC Cys	CCA Pro	GAG Glu	1104

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Ser 350	Thr	Cys	Ile	Asp	Arg 355	Val	Ala	Ser	Phe	Ser 360	Cys	Met	Cys	Pro	Glu 365	
GGG Gly	AAG Lys	GCA Ala	GGT Gly	CTC Leu 370	CTG Leu	TGT Cys	CAT His	CTG Leu	GAT Asp 375	GAT Asp	GCA Ala	TGC Cys	ATC Ile	AGC Ser 380	AAT Asn	1152
CCT Pro	TGC Cys	CAC His	AAG Lys 385	GGG Gly	GCA Ala	CTG Leu	TGT Cys	GAC Asp 390	ACC Thr	AAC Asn	CCC Pro	CTA Leu	AAT Asn 395	GGG Gly	CAA Gln	1200
TAT Tyr	ATT Ile	TGC Cys 400	ACC Thr	TGC Cys	CCA Pro	CAA Gln	GGC Gly 405	TAC Tyr	AAA Lys	GGG Gly	GCT Ala 410	GAC Cys	TGC Thr	ACA Glu	GAA Glu	1248
GAT Asp 415	GTG Val	GAT Asp	GAA Glu	TGT Cys	GCC Ala	ATG Met 420	GCC Ala	AAT Asn	AGC Ser	AAT Asn	CCT Pro 425	TGT Cys	GAG Glu	CAT His	GCA Ala	1296
GGA Gly 430	AAA Lys	TGT Cys	GTG Val	AAC Asn 435	ACG Thr	GAT Asp	GGC Gly	GCC Ala	TTC Phe	CAC His 440	TGT Cys	GAG Glu	TGT Cys	CTG Leu	AAG Lys 445	1344
GGT Gly	TAT Tyr	GCA Ala	GGA Gly	CCT Pro 450	CGT Arg	TGT Cys	GAG Glu	ATG Met	GAC Asp 455	ATC Ile	AAT Asn	GAG Glu	TGC Cys	CAT His 460	TCA Ser	1392
GAC Asp	CCC Pro	TGC Cys	CAG Gln 465	AAT Asn	GAT Asp	GCT Ala	ACC Thr	TGT Cys 470	CTG Leu	GAT Asp	AAG Lys	ATT Ile	GGA Gly 475	GGC Gly	TTC Phe	1440
ACA Thr	TGT Cys	CTG Leu 480	TGC Cys	ATG Met	CCA Pro	GGT Gly	TTC Phe 485	AAA Lys	GGT Gly	GTG Val	CAT His	TGT Cys 490	GAA Glu	TTA Leu	GAA Glu	1488
ATA Ile 495	AAT Asn	GAA Glu	TGT Cys	CAG Gln	AGC Ser	AAC Asn 500	CCT Pro	TGT Cys	GTG Val	AAC Asn	AAT Asn 505	GGG Gly	CAG Gln	TGT Cys	GTG Val	1536
GAT Asp 510	AAA Lys	GTC Val	AAT Asn	CGT Arg	TTC Phe 515	CAG Gln	TGC Cys	CTG Leu	TGT Cys	CCT Pro 520	CCT Pro	GGT Gly	TTC Phe	ACT Thr	GGG Gly 525	1584
CCA Pro	GTT Val	TGC Cys	CAG Gln 530	ATT Ile	GAT Asp	ATT Ile	GAT Asp	GAC Asp	TGT Cys 535	TCC Ser	AGT Ser	ACT Thr	CCG Pro	TGT Cys 540	CTG Leu	1632
AAT Asn	GGG Gly	GCA Ala	AAG Lys 545	TGT Cys	ATC Ile	GAT Asp	CAC His	CCG Pro 550	AAT Asn	GGC Gly	TAT Tyr	GAA Glu	TGC Cys 555	CAG Gln	TGT Cys	1680
GCC Ala	ACA Thr	GGT Gly 560	TTC Phe	ACT Thr	GGT Gly	GTG Val	TTG Leu 565	TGT Cys	GAG Glu	GAG Glu	AAC Asn	ATT Ile 570	GAC Asp	AAC Asn	TGT Cys	1728
GAC Asp 575	CCC Pro	GAT Asp	CCT Pro	TGC Cys	CAC His	CAT His 580	GGT Gly	CAG Gln	TGT Cys	CAG Gln	GAT Asp 585	GGT Gly	ATT Ile	GAT Asp	TCC Ser	1776
TAC Tyr 590	ACC Thr	TGC Cys	ATC Ile	TGC Cys	AAT Asn 595	CCC Pro	GGG Gly	TAC Tyr	ATG Met	GGC Gly 600	GCC Ala	ATC Ile	TGC Cys	AGT Ser	GAC Asp 605	1824
CAG Gln	ATT Ile	GAT Asp	GAA Glu	TGT Cys 610	TAC Tyr	AGC Ser	AGC Ser	CCT Pro	TGC Cys 615	CTG Leu	AAC Asn	GAT Asp	GGT Gly	CGC Arg 620	TGC Cys	1872

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ATT Ile	GAC Asp	CTG Leu	GTC Val 625	AAT Asn	GGC Gly	TAC Tyr	CAG Gln	TGC Cys 630	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GGC Gly 635	ACG Thr	TCA Ser	1920
GGG Gly	GTT Val	AAT Asn 640	TGT Cys	GAA Glu	ATT Ile	AAT Asn	TTT Phe 645	GAT Asp	GAC Asp	TGT Cys	GCA Ala	AGT Ser 650	AAC Asn	CCT Pro	TGT Cys	1968
ATC Ile	CAT His 655	GGA Gly	ATC Ile	TGT Cys	ATG Met	GAT Asp 660	GGC Gly	ATT Ile	AAT Asn	CGC Arg	TAC Tyr 665	AGT Ser	TGT Cys	GTC Val	TGC Cys	2016
TCA Ser 670	CCA Pro	GGA Gly	TTC Phe	ACA Thr	GGG Gly 675	CAG Gln	AGA Arg	TGT Cys	AAC Asn	ATT Ile 680	GAC Asp	ATT Ile	GAT Asp	GAG Glu	TGT Cys 685	2064
GCC Ala	TCC Ser	AAT Asn	CCC Pro	TGT Cys 690	CGC Arg	AAG Lys	GGT Gly	GCA Ala	ACA Thr 695	TGT Cys	ATC Ile	AAC Asn	GGT Gly	GTG Val 700	AAT Asn	2112
GGT Gly	TTC Phe	CGC Arg 705	TGT Cys	ATA Ile	TGC Cys	CCC Pro	GAG Glu	GGA Gly 710	CCC Pro	CAT His	CAC His	CCC Pro	AGC Ser 715	TGC Cys	TAC Tyr	2160
TCA Ser	CAG Gln	GTG Val 720	AAC Asn	GAA Glu	TGC Cys	CTG Leu 725	AGC Ser	AAT Asn	CCC Pro	TGC Cys	ATC Ile	CAT His 730	GGA Gly	AAC Asn	TGT Cys	2208
B ACT Thr	GGA Gly 735	GGT Gly	CTC Leu	AGT Ser	GGA Gly	TAT Tyr 740	AAG Lys	TGT Cys	CTC Leu	TGT Cys	GAT Asp 745	GCA Ala	GGC Gly	TGG Trp	GTT Val	2256
GGC Gly 750	ATC Ile	AAC Asn	TGT Cys	GAA Glu	GTG Val 755	GAC Asp	AAA Lys	AAT Asn	GAA Glu	TGC Cys 760	CTT Leu	TCG Ser	AAT Asn	CCA Pro	TGC Cys 765	2304
CAG Gln	AAT Asn	GGA Gly	GGA Gly	ACT Thr 770	TGT Cys	GAC Asp	AAT Asn	CTG Leu	GTG Val 775	AAT Asn	GGA Gly	TAC Tyr	AGG Arg	TGT Cys 780	ACT Thr	2352
TGC Cys	AAG Lys	AAG Lys	GGC Gly 785	TTT Phe	AAA Lys	GGC Gly	TAT Tyr	AAC Asn 790	TGC Cys	CAG Gln	GTG Val	AAT Asn	ATT Ile 795	GAT Asp	GAA Glu	2400
TGT Cys	GCC Ala	TCA Ser 800	AAT Asn	CCA Pro	TGC Cys	CTG Leu	AAC Asn 805	CAA Gln	GGA Gly	ACC Thr	TGC Cys	TTT Phe 810	GAT Asp	GAC Asp	ATA Ile	2448
AGT Ser	GGC Gly 815	TAC Tyr	ACT Thr	TGC Cys	CAC His	TGT Cys 820	GTG Val	CTG Leu	CCA Pro	TAC Tyr	ACA Thr 825	GGC Gly	AAG Lys	AAT Asn	TGT Cys	2496
CAG Gln 830	ACA Thr	GTA Val	TTG Leu	GCT Ala	CCC Pro 835	TGT Cys	TCC Ser	CCA Pro	AAC Asn	CCT Pro 840	TGT Cys	GAG Glu	AAT Asn	GCT Ala	GCT Ala 845	2544
GTT Val	TGC Cys	AAA Lys	GAG Glu	TCA Ser 850	CCA Pro	AAT Asn	TTT Phe	GAG Glu	AGT Ser 855	TAT Tyr	ACT Thr	TGC Cys	TTG Leu	TGT Cys 860	GCT Ala	2592
CCT Pro	GGC Gly	TGG Trp	CAA Gln 865	GGT Gly	CAG Gln	CGG Arg	TGT Cys	ACC Thr 870	ATT Ile	GAC Asp	ATT Ile	GAC Asp	GAG Glu 875	TGT Cys	ATC Ile	2640
TCC Ser	AAG Lys	CCC Pro 880	TGC Cys	ATG Met	AAC Asn	CAT His	GGT Gly 885	CTC Leu	TGC Cys	CAT His	AAC Asn	ACC Thr 890	CAG Gln	GGC Gly	AGC Ser	2688

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TAC Tyr 895	ATG Met	TGT Cys	GAA Glu	TGT Cys	CCA Pro	CCA Pro 900	GGC Gly	TTC Phe	AGT Ser	GGT Gly	ATG Met 905	GAC Asp	TGT Cys	GAG Glu	GAG Glu	2736
GAC Asp 910	ATT Ile	GAT Asp	GAC Asp	TGC Cys	CTT Leu 915	GCC Ala	AAT Asn	CCT Pro	TGC Cys	CAG Gln 920	AAT Asn	GGA Gly	GGT Gly	TCC Ser	TGT Cys 925	2784
ATG Met	GAT Asp	GGA Gly	GTG Val	AAT Asn 930	ACT Thr	TTC Phe	TCC Ser	TGC Cys	CTC Leu 935	TGC Cys	CTT Leu	CCG Pro	GGT Gly	TTC Phe 940	ACT Thr	2832
GGG Gly	GAT Asp	AAG Lys	TGC Cys 945	CAG Gln	ACA Thr	GAC Asp	ATG Met	AAT Asn 950	GAG Glu	TGT Cys	CTG Leu	AGT Ser	GAA Glu 955	CCC Pro	TGT Cys	2880
AAG Lys	AAT Asn 960	GGA Gly	GGG Gly	ACC Thr	TGC Cys	TCT Ser	GAC Asp 965	TAC Tyr	GTC Val	AAC Asn	AGT Ser	TAC Tyr 970	ACT Thr	TGC Cys	AAG Lys	2928
TGC Cys 975	CAG Gln	GCA Ala	GGA Gly	TTT Phe	GAT Asp	GGA Gly 980	GTC Val	CAT His	TGT Cys	GAG Glu	AAC Asn 985	AAC Asn	ATC Ile	AAT Asn	GAG Glu	2976
TGC Cys 990	ACT Thr	GAG Glu	AGC Ser	TCC Ser	TGT Cys 995	TTC Phe	AAT Asn	GGT Gly	GGC Gly	ACA Thr 1000	TGT Cys	GTT Val	GAT Asp	GGG Gly	ATT Ile 1005	3024
AAC Asn	TCC Ser	TTC Phe	TCT Ser	TGC Cys 1010	TTG Leu	TGC Cys	CCT Pro	GTG Val	GGT Gly 1015	TTC Phe	ACT Thr	GGA Gly	TCC Ser	TTC Phe 1020	TGC Cys	3072
CTC Leu	CAT His	GAG Glu	ATC Ile	AAT Asn	GAA Glu	TGC Cys	AGC Ser	TCT Ser	CAT His	CCA Pro	TGC Cys	CTG Leu	AAT Asn	GAG Glu	GGA Gly	3120
ACG Thr	TGT Cys	GTT Val	GAT Asp	GGC Gly	CTG Leu	GGT Gly	ACC Thr	TAC Tyr	CGC Arg	TGC Cys	AGC Ser	TGC Cys	CCC Pro	CTG Leu	GGC Gly	3168
TAC Tyr	ACT Thr	GGG Gly	AAA Lys	AAC Asn	TGT Cys	CAG Gln	ACC Thr	CTG Leu	GTG Val	AAT Asn	CTC Leu	TGC Cys	AGT Ser	CGG Arg	TCT Ser	3216
CCA Pro 1070	TGT Cys	AAA Lys	AAC Asn	AAA Lys	GGT Gly 1075	ACT Thr	TGT Cys	GTT Val	CAG Gln	AAA Lys 1080	AAA Lys	GCA Ala	GAG Glu	TCC Ser	CAG Gln 1085	3264
TGC Cys	CTA Leu	TGT Cys	CCA Pro	TCT Ser 1090	GGA Gly	TGG Trp	GCT Ala	GGT Gly	GCC Ala	TAT Tyr 1095	TGT Cys	GAC Asp	GTG Val	CCC Pro 1100	AAT Asn	3312
GTC Val	TCT Ser	TGT Cys	GAC Asp	ATA Ile 1105	GCA Ala	GCC Ala	TCC Ser	AGG Arg	AGA Arg	GGT Gly	GTG Val	CTT Leu	GTT Val	GAA Glu 1115	CAC His	3360
TTG Leu	TGC Cys	CAG Gln	CAC His	TCA Ser	GGT Gly	GTC Val	TGC Cys	ATC Ile	AAT Asn	GCT Ala	GGC Gly	AAC Asn	ACG Thr	CAT His	TAC Tyr	3408
TGT Cys 1135	CAG Gln	TGC Cys	CCC Pro	CTG Leu	GGC Gly	TAT Tyr	ACT Thr	GGG Gly	AGC Ser	TAC Tyr	TGT Cys	GAG Glu	GAG Glu	CAA Gln	CTC Leu	3456
GAT Asp 1150	GAG Glu	TGT Cys	GCG Ala	TCC Ser	AAC Asn	CCC Pro	TGC Cys	CAG Gln	CAC His	GGG Gly 1160	GCA Ala	ACA Thr	TGC Cys	AGT Ser	GAC Asp 1165	3504

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TTC ATT GGT GGA TAC AGA TGC GAG TGT GTC CCA GGC TAT CAG GGT GTC	3552
Phe Ile Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val	
1170 1175 1180	
AAC TGT GAG TAT GAA GTG GAT GAG TGC CAG AAT CAG CCC TGC CAG AAT	3600
Asn Cys Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn	
1185 1190 1195	
GGA GGC ACC TGT ATT GAC CTT GTG AAC CAT TTC AAG TGC TCT TGC CCA	3648
Gly Gly Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro	
1200 1205 1210	
CCA GGC ACT CGG GGC CTA CTC TGT GAA GAG AAC ATT GAT GAC TGT GCC	3696
Pro Gly Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala	
1215 1220 1225	
CGG GGT CCC CAT TGC CTT AAT GGT GGT CAG TGC ATG GAT AGG ATT GGA	3744
Arg Gly Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly	
1230 1235 1240 1245	
GGC TAC AGT TGT CGC TGC TTG CCT GGC TTT GCT GGG GAG CGT TGT GAG	3792
Gly Tyr Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu	
1250 1255 1260	
GGA GAC ATC AAC GAG TGC CTC TCC AAC CCC TGC AGC TCT GAG GGC AGC	3840
Gly Asp Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser	
1265 1270 1275	
CTG GAC TGT ATA CAG CTC ACC AAT GAC TAC CTG TGT GTT TGC CGT AGT	3888
Leu Asp Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser	
1280 1285 1290	
GCC TTT ACT GGC CGG CAC TGT GAA ACC TTC GTC GAT GTG TGT CCC CAG	3936
Ala Phe Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln	
1295 1300 1305	
ATG CCC TGC CTG AAT GGA GGG ACT TGT GCT GTG GCC AGT AAC ATG CCT	3984
Met Pro Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro	
1310 1315 1320 1325	
GAT GGT TTC ATT TGC CGT TGT CCC CCG GGA TTT TCC GGG GCA AGG TGC	4032
Asp Gly Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys	
1330 1335 1340	
CAG AGC AGC TGT GGA CAA GTG AAA TGT AGG AAG GGG GAG CAG TGT GTG	4080
Gln Ser Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val	
1345 1350 1355	
CAC ACC GCC TCT GGA CCC GGC TGC TTC TGC CCC AGT CCC CGG GAC TGC	4128
His Thr Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys	
1360 1365 1370	
GAG TCA GGC TGT GCC AGT AGC CCC TGC CAG CAC GGG GGC AGC TGC CAC	4176
Glu Ser Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His	
1375 1380 1385	
CCT CAG CGC CAG CCT CCT TAT TAC TCC TGC CAG TGT GCC CCA CCA TTC	4224
Pro Gln Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro Phe	
1390 1395 1400 1405	
TCG GGT AGC CGC TGT GAA CTC TAC ACG GCA CCC CCC AGC ACC CCT CCT	4272
Ser Gly Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr Pro Pro	
1410 1415 1420	
GCC ACC TGT CTG AGC CAG TAT TGT GCC GAC AAA GCT CGG GAT GGC GTC	4320
Ala Thr Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val	
1425 1430 1435	

B

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TGT GAT GAG GCC TGC AAC AGC CAT GCC TGC CAG TGG GAT GGG GGT GAC Cys Asp Glu Ala Cys Asn Ser His Ala Cys Gln Trp Asp Gly Gly Asp 1440 1445 1450	4368
TGT TCT CTC ACC ATG GAG AAC CCC TGG GCC AAC TGC TCC TCC CCA CTT Cys Ser Leu Thr Met Glu Asn Pro Trp Ala Asn Cys Ser Ser Pro Leu 1455 1460 1465	4416
CCC TGC TGG GAT TAT ATC AAC AAC CAG TGT GAT GAG CTG TGC AAC ACG Pro Cys Trp Asp Tyr Ile Asn Asn Gln Cys Asp Glu Leu Cys Asn Thr 1470 1475 1480 1485	4464
GTC GAG TGC CTG TTT GAC AAC TTT GAA TGC CAG GGG AAC AGC AAG ACA Val Glu Cys Leu Phe Asp Asn Phe Glu Cys Gln Gly Asn Ser Lys Thr 1490 1495 1500	4512
TGC AAG TAT GAC AAA TAC TGT GCA GAC CAC TTC AAA GAC AAC CAC TGT Cys Lys Tyr Asp Lys Tyr Cys Ala Asp His Phe Lys Asp Asn His Cys 1505 1510 1515	4560
AAC CAG GGG TGC AAC AGT GAG GAG TGT GGT TGG GAT GGG CTG GAC TGT Asn Gln Gly Cys Asn Ser Glu Glu Cys Gly Trp Asp Gly Leu Asp Cys 1520 1525 1530	4608
GCT GCT GAC CAA CCT GAG AAC CTG GCA GAA GGT ACC CTG GTT ATT GTG Ala Ala Asp Gln Pro Glu Asn Leu Ala Glu Gly Thr Leu Val Ile Val 1535 1540 1545	4656
GTA TTG ATG CCA CCT GAA CAA CTG CTC CAG GAT GCT CGC AGC TTC TTG Val Leu Met Pro Pro Glu Gln Leu Leu Gln Asp Ala Arg Ser Phe Leu 1550 1555 1560 1565	4704
CGG GCA CTG GGT ACC CTG CTC CAC ACC AAC CTG CGC ATT AAG CGG GAC Arg Ala Leu Gly Thr Leu Leu His Thr Asn Leu Arg Ile Lys Arg Asp 1570 1575 1580	4752
TCC CAG GGG GAA CTC ATG GTG TAC CCC TAT TAT GGT GAG AAG TCA GCT Ser Gln Gly Glu Leu Met Val Tyr Pro Tyr Tyr Gly Glu Lys Ser Ala 1585 1590 1595	4800
GCT ATG AAG AAA CAG AGG ATG ACA CGC AGA TCC CTT CCT GGT GAA CAA Ala Met Lys Lys Gln Arg Met Thr Arg Arg Ser Leu Pro Gly Glu Gln 1600 1605 1610	4848
GAA CAG GAG GTG GCT GGC TCT AAA GTC TTT CTG GAA ATT GAC AAC CGC Glu Gln Glu Val Ala Gly Ser Lys Val Phe Leu Ile Asp Asn Arg 1615 1620 1625	4896
CAG TGT GTT CAA GAC TCA GAC CAC TGC TTC AAG AAC ACG GAT GCA GCA Gln Cys Val Gln Asp Ser Asp His Cys Phe Lys Asn Thr Asp Ala Ala 1630 1635 1640 1645	4944
GCA GCT CTC CTG GCC TCT CAC GCC ATA CAG GGG ACC CTG TCA TAC CCT Ala Ala Leu Leu Ala Ser His Ala Ile Gln Gly Thr Leu Ser Tyr Pro 1650 1655 1660	4992
CTT GTG TCT GTC GTC AGT GAA TCC CTG ACT CCA GAA CGC ACT CAG CTC Leu Val Ser Val Val Ser Glu Ser Leu Thr Pro Glu Arg Thr Gln Leu 1665 1670 1675	5040
CTC TAT CTC CTT GCT GTT GCT GTT GTC ATC ATT CTG TTT ATT ATT CTG Leu Tyr Leu Leu Ala Val Ala Val Val Ile Ile Leu Phe Ile Ile Leu 1680 1685 1690	5088
CTG GGG GTA ATC ATG GCA AAA CGA AAG CGT AAG CAT GGC TCT CTC TGG Leu Gly Val Ile Met Ala Lys Arg Lys Arg Lys His Gly Ser Leu Trp 1695 1700 1705	5136

B

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CTG CCT GAA GGT TTC ACT CTT CGC CGA GAT GCA AGC AAT CAC AAG CGT Leu Pro Glu Gly Phe Thr Leu Arg Arg Asp Ala Ser Asn His Lys Arg 1710 1715 1720 1725	5184
CGT GAG CCA GTG GGA CAG GAT GCT GTG GGG CTG AAA AAT CTC TCA GTG Arg Glu Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val 1730 1735 1740	5232
CAA GTC TCA GAA GCT AAC CTA ATT GGT ACT GGA ACA AGT GAA CAC TGG Gln Val Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp 1745 1750 1755	5280
GTC GAT GAT GAA GGG CCC CAG CCA AAG AAA GTA AAG GCT GAA GAT GAG Val Asp Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu 1760 1765 1770	5328
GCC TTA CTC TCA GAA GAA GAT GAC CCC ATT GAT CGA CGG CCA TGG ACA Ala Leu Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr 1775 1780 1785	5376
CAG CAG CAC CTT GAA GCT GCA GAC ATC CGT AGG ACA CCA TCG CTG GCT Gln Gln His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala 1790 1795 1800 1805	5424
CTC ACC CCT CCT CAG GCA GAG CAG GAG GTG GAT GTG TTA GAT GTG AAT Leu Thr Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn 1810 1815 1820	5472
GTC CGT GGC CCA GAT GGC TGC ACC CCA TTG ATG TTG GCT TCT CTC CGA Val Arg Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg 1825 1830 1835	5520
GGA GGC AGC TCA GAT TTG AGT GAT GAA GAT GAA GAT GCA GAG GAC TCT Gly Gly Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser 1840 1845 1850	5568
TCT GCT AAC ATC ATC ACA GAC TTG GTC TAC CAG GGT GCC AGC CTC CAG Ser Ala Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln 1855 1860 1865	5616
GCC CAG ACA GAC CGG ACT GGT GAG ATG GCC CTG CAC CTT GCA GCC CGC Ala Gln Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg 1870 1875 1880 1885	5664
TAC TCA CGG GCT GAT GCT GCC AAG CGT CTC CTG GAT GCA GGT GCA GAT Tyr Ser Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp 1890 1895 1900	5712
GCC AAT GCC CAG GAC AAC ATG GGC CGC TGT CCA CTC CAT GCT GCA GTG Ala Asn Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val 1905 1910 1915	5760
GCA GCT GAT GCC CAA GGT GTC TTC CAG ATT CTG ATT CGC AAC CGA GTA Ala Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val 1920 1925 1930	5808
ACT GAT CTA GAT GCC AGG ATG AAT GAT GGT ACT ACA CCC CTG ATC CTG Thr Asp Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu 1935 1940 1945	5856
GCT GCC CGC CTG GCT GTG GAG GGA ATG GTG GCA GAA CTG ATC AAC TGC Ala Ala Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys 1950 1955 1960 1965	5904
CAA GCG GAT GTG AAT GCA GTG GAT GAC CAT GGA AAA TCT GCT CTT CAC Gln Ala Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His 1970 1975 1980	5952

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TGG	GCA	GCT	GCT	GTC	AAT	AAT	GTG	GAG	GCA	ACT	CTT	TTG	TTG	TTG	AAA	6000
Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Glu	Ala	Thr	Leu	Leu	Leu	Leu	Lys	
			1985					1990				1995				
AAT	GGG	GCC	AAC	CGA	GAC	ATG	CAG	GAC	AAC	AAG	GAA	GAG	ACA	CCT	CTG	6048
Asn	Gly	Ala	Asn	Arg	Asp	Met	Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	
		2000					2005				2010					
TTT	CTT	GCT	GCC	CGG	GAG	GGG	AGC	TAT	GAA	GCA	GCC	AAG	ATC	CTG	TTA	6096
Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	
	2015					2020					2025					
GAC	CAT	TTT	GCC	AAT	CGA	GAC	ATC	ACA	GAC	CAT	ATG	GAT	CGT	CTT	CCC	6144
Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	
2030					2035					2040					2045	
CGG	GAT	GTG	GCT	CGG	GAT	CGC	ATG	CAC	CAT	GAC	ATT	GTG	CGC	CTT	CTG	6192
Arg	Asp	Val	Ala	Arg	Asp	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	
				2050						2055				2060		
GAT	GAA	TAC	AAT	GTG	ACC	CCA	AGC	CCT	CCA	GGC	ACC	GTG	TTG	ACT	TCT	6240
Asp	Glu	Tyr	Asn	Val	Thr	Pro	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	
			2065					2070				2075				
GCT	CTC	TCA	CCT	GTC	ATC	TGT	GGG	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTG	6288
Ala	Leu	Ser	Pro	Val	Ile	Cys	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	
		2080					2085					2090				
AAG	CAC	ACC	CCA	ATG	GGC	AAG	AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	6336
Lys	His	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	
	2095					2100					2105					
ACC	ATG	CCT	ACT	AGC	CTC	CCT	AAC	CTT	GCC	AAG	GAG	GCA	AAG	GAT	GCC	6384
Thr	Met	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	
2110					2115					2120					2125	
AAG	GGT	AGT	AGG	AGG	AAG	AAG	TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	6432
Lys	Gly	Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	
				2130					2135				2140			
GAG	AGT	TCA	GTA	ACT	TTA	TCC	CCT	GTT	GAT	TCC	CTA	GAA	TCT	CCT	CAC	6480
Glu	Ser	Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	
			2145					2150				2155				
ACG	TAT	GTT	TCC	GAC	ACC	ACA	TCC	TCT	CCA	ATG	ATT	ACA	TCC	CCT	GGG	6528
Thr	Tyr	Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	
		2160					2165					2170				
ATC	TTA	CAG	GCC	TCA	CCC	AAC	CCT	ATG	TTG	GCC	ACT	GCC	GCC	CCT	CCT	6576
Ile	Leu	Gln	Ala	Ser	Pro	Asn	Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	
	2175					2180					2185					
GCC	CCA	GTC	CAT	GCC	CAG	CAT	GCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	6624
Ala	Pro	Val	His	Ala	Gln	His	Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	
2190					2195					2200					2205	
ATG	CAG	CCT	TTG	GCA	CAT	GGG	GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	6672
Met	Gln	Pro	Leu	Ala	His	Gly	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	
				2210					2215					2220		
CAG	TTG	CTA	TCC	CAC	CAC	CAC	ATT	GTG	TCT	CCA	GGC	AGT	GGC	AGT	GCT	6720
Gln	Leu	Leu	Ser	His	His	His	Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	
			2225					2230					2235			
GGA	AGC	TTG	AGT	AGG	CTC	CAT	CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATG	6768
Gly	Ser	Leu	Ser	Arg	Leu	His	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	
		2240					2245					2250				

AAC CGC ATG GAG GTG AAT GAG ACC CAG TAC AAT GAG ATG TTT GGT ATG Asn Arg Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly Met 2255 2260 2265	6816
GTC CTG GCT CCA GCT GAG GGC ACC CAT CCT GGC ATA GCT CCC CAG AGC Val Leu Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser 2270 2275 2280 2285	6864
AGG CCA CCT GAA GGG AAG CAC ATA ACC ACC CCT CGG GAG CCC TTG CCC Arg Pro Pro Glu Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro 2290 2295 2300	6912
CCC ATT GTG ACT TTC CAG CTC ATC CCT AAA GGC AGT ATT GCC CAA CCA Pro Ile Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro 2305 2310 2315	6960
GCG GGG GCT CCC CAG CCT CAG TCC ACC TGC CCT CCA GCT GTT GCG GGC Ala Gly Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly 2320 2325 2330	7008
CCC CTG CCC ACC ATG TAC CAG ATT CCA GAA ATG GCC CGT TTG CCC AGT Pro Leu Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser 2335 2340 2345	7056
GTG GCT TTC CCC ACT GCC ATG ATG CCC CAG CAG GAC GGG CAG GTA GCT Val Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala 2350 2355 2360 2365	7104
CAG ACC ATT CTC CCA GCC TAT CAT CCT TTC CCA GCC TCT GTG GGC AAG Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys 2370 2375 2380	7152
TAC CCC ACA CCC CCT TCA CAG CAC AGT TAT GCT TCC TCA AAT GCT GCT Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala 2385 2390 2395	7200
GAG CGA ACA CCC AGT CAC AGT GGT CAC CTC CAG GGT GAG CAT CCC TAC Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr 2400 2405 2410	7248
CTG ACA CCA TCC CCA GAG TCT CCT GAC CAG TGG TCA AGT TCA TCA CCC Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Pro 2415 2420 2425	7296
CAC TCT GCT TCT GAC TGG TCA GAT GTG ACC ACC AGC CCT ACC CCT GGG His Ser Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly 2430 2435 2440 2445	7344
GGT GCT GGA GGA GGT CAG CGG GGA CCT GGG ACA CAC ATG TCT GAG CCA Gly Ala Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro 2450 2455 2460	7392
CCA CAC AAC AAC ATG CAG GTT TAT GCG TGAGAGAGTC CACCTCCAGT Pro His Asn Asn Met Gln Val Tyr Ala 2465 2470	7439
GTAGAGACAT AACTGACTTT TGTAATGCT GCTGAGGAAC AAATGAAGGT CATCCGGGAG	7499
AGAAATGAAG AAATCTCTGG AGCCAGCTTC TAGAGGTAGG AAAGAGAAGA TGTTCTTATT	7559
CAGATAATGC AAGAGAAGCA ATTCGTCAGT TTCACTGGGT ATCTGCAAGG CTTATTGATT	7619
ATTCTAATCT AATAAGACAA GTTTGTGGAA ATGCAAGATG AATACAAGCC TTGGGTCCAT	7679
GTTTACTCTC TTCTATTTGG AGAATAAGAT GGATGCTTAT TGAAGCCCAG ACATTCTTGC	7739
AGCTTGGACT GCATTTTAAG CCCTGCAGGC TTCTGCCATA TCCATGAGAA GATTCTACAC	7799



TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA	TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	7859
CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG	TGCTTTTGGT	TTTGACCTC	TCCGTGATTG	7919
TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC	CTTTGTGCTT	TTGATCATTC	TGGCCCATGA	7979
AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	8039
TTTACTTTGG	TATGGTTCTC	AGCACAAACC	TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	8099
ACATACTGTA	TTGTGTTCTC	CTGCATATAT	CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	8159
CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	8219
CTTGTCTGTG	TGCAGGTCTT	CATATAAACT	TTACCAGGAA	GAAGGGTGTG	AGTTTGTGTG	8279
TTTTCTGTGT	ATGGGCCTGG	TCAGTGTAAG	GTTTTATCCT	TGATAGTCTA	GTTACTATGA	8339
CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	GTTTGGAATG	TTGGAATGAC	CAAGAGACAA	8399
GTAACTCGT	GCAAGAGCCA	GTTACCCACC	CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	8459
CCATTGACTG	CCTGTATGGA	ACACATTTGT	CCCAGATCTG	AGCATTCTAG	GCCTGTTTCA	8519
CTCACTCACC	CAGCATATGA	AACTAGTCTT	AACTGTTGAG	CCTTTCCTTT	CATATCCACA	8579
GAAGACACTG	TCTCAAATGT	TGTACCCCTG	CCATTTAGGA	CTGAACTTTC	CTTAGCCCAA	8639
GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	8699
TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	8759
CCCAGTATGT	TCTCACTGAA	GACATGGACT	TTATATGTTT	AAGTGCAGGA	ATTGGAAAAGT	8819
TGGACTTGTT	TTCTATGATC	CAAAACAGCC	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	8879
ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	8939
CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	8999
GATGATAATG	GACAACTATA	GACTTGCTCA	TTGTTGAGAC	TGATTGCCCC	TCACCTGAAT	9059
CCACTCTCTG	TATTCATGCT	CTTGGCAATT	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	9119
TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	9179
TGGTCCATGG	CTCACTGCA	ACTTCCGTCC	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	9239
TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	9299
AATGACAGTT	CTCATTCCTT	CTATGGCTGC	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	9359
ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	9419
AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	TGAACCAACA	AAAATAATTA	CTTCTGCCCT	9479
GAGATAAGCA	GATTAAGTTT	GTTCAATTCT	TGCTTTATTC	TCTCCATGTG	GCAACATTCT	9539
GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	TATCATTCTA	AATGGTGACT	CTCTGCCCTT	9599
GGACCCATTT	ATTATTCACA	GATGGGGAGA	ACCTATCTGC	ATGGACCCTC	ACCATCCTCT	9659
GTGCAGCACA	CACAGTGCAG	GGAGCCAGTG	GCGATGGCGA	TGACTTTCTT	CCCCTGGGAA	9719
TTCC						9723

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